

<110> Connaught Laboratories Limited

<120> Chlamydia antigens and corresponding DNA fragments and uses thereof

<130> 77813-5

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<151> December 23, 1998

<150> 60/114,050

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<151> December 28, 1998

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<170> PatentIn Ver. 2.0

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Pro Thr Ser Gly Ser Ser Thr Pro Val Pro Ile Val Thr Phe Ser Asp	
265 270 275	
aat aaa cag tta gtc ttt gaa aga aac cat tcc ata atg ggt ggc gga	979
Asn Lys Gln Leu Val Phe Glu Arg Asn His Ser Ile Met Gly Gly Gly	
280 285 290	
gcc att tat gct agg aaa ctt agc atc tct tca gga ggt cct act cta	1027
Ala Ile Tyr Ala Arg Lys Leu Ser Ile Ser Ser Gly Gly Pro Thr Leu	
295 300 305	
ttt atc aat aat ata tca tat gca aat tcg caa aat tta ggt gga gct	1075
Phe Ile Asn Asn Ile Ser Tyr Ala Asn Ser Gln Asn Leu Gly Gly Ala	
310 315 320 325	
att gcc att gat act gga ggg gag atc agt tta tca gca gag aaa gga	1123
Ile Ala Ile Asp Thr Gly Gly Glu Ile Ser Leu Ser Ala Glu Lys Gly	
330 335 340	
aca att aca ttc caa gga aac cgg acg agc tta ccg ttt ttg aat ggc	1171
Thr Ile Thr Phe Gln Gly Asn Arg Thr Ser Leu Pro Phe Leu Asn Gly	
345 350 355	

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atc cat ctt tta caa aat gct aaa ttc ctg aaa tta cag gcg aga aat 1219  
 Ile His Leu Leu Gln Asn Ala Lys Phe Leu Lys Leu Gln Ala Arg Asn  
 360 365 370

gga tac tct ata gaa ttt tat gat cct att act tct gaa gca gat ggg 1267  
 Gly Tyr Ser Ile Glu Phe Tyr Asp Pro Ile Thr Ser Glu Ala Asp Gly  
 375 380 385

tct acc caa ttg aat atc aac gga gat cct aaa aat aaa gag tac aca 1315  
 Ser Thr Gln Leu Asn Ile Asn Gly Asp Pro Lys Asn Lys Glu Tyr Thr  
 390 395 400 405

ggg acc ata ctc ttt tct gga gaa aag agt cta gca aac gat cct agg 1363  
 Gly Thr Ile Leu Phe Ser Gly Glu Lys Ser Leu Ala Asn Asp Pro Arg  
 410 415 420

gat ttt aaa tct aca atc cct cag aac gtc aac ctg tct gca gga tac 1411  
 Asp Phe Lys Ser Thr Ile Pro Gln Asn Val Asn Leu Ser Ala Gly Tyr  
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tta gtt att aaa gag ggg gcc gaa gtc aca gtt tca aaa ttc acg cag 1459  
 Leu Val Ile Lys Glu Gly Ala Glu Val Thr Val Ser Lys Phe Thr Gln  
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tct cca gga tcg cat tta gtt tta gat tta gga acc aaa ctg ata gcc 1507  
 Ser Pro Gly Ser His Leu Val Leu Asp Leu Gly Thr Lys Leu Ile Ala  
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tct aag gaa gac att gcc atc aca ggc ctc gcg ata gat ata gat agc 1555  
 Ser Lys Glu Asp Ile Ala Ile Thr Gly Leu Ala Ile Asp Ile Asp Ser  
 470 475 480 485

tta agc tca tcc tca aca gca gct gtt att aaa gca aac acc gca aat 1603  
 Leu Ser Ser Ser Ser Thr Ala Ala Val Ile Lys Ala Asn Thr Ala Asn  
 490 495 500

aaa cag ata tcc gtg acg gac tct ata gaa ctt atc tcg cct act ggc 1651  
 Lys Gln Ile Ser Val Thr Asp Ser Ile Glu Leu Ile Ser Pro Thr Gly  
 505 510 515

aat gcc tat gaa gat ctc aga atg aga aat tca cag acg ttc cct ctg 1699  
 Asn Ala Tyr Glu Asp Leu Arg Met Arg Asn Ser Gln Thr Phe Pro Leu  
 520 525 530

ctc tct tta gag cct gga gcc ggg ggt agt gtg act gta act gct gga 1747  
 Leu Ser Leu Glu Pro Gly Ala Gly Gly Ser Val Thr Val Thr Ala Gly  
 535 540 545

gat ttc cta ccg gta agt ccc cat tat ggt ttt caa ggc aat tgg aaa 1795  
 Asp Phe Leu Pro Val Ser Pro His Tyr Gly Phe Gln Gly Asn Trp Lys  
 550 555 560 565

14/55

tta gct tgg aca gga act gga aac aaa gtt gga gaa ttc ttc tgg gat	1843
Leu Ala Trp Thr Gly Thr Gly Asn Lys Val Gly Glu Phe Phe Trp Asp	
570 575 580	
aaa ata aat tat aag cct aga cct gaa aaa gaa gga aat tta gtt cct	1891
Lys Ile Asn Tyr Lys Pro Arg Pro Glu Lys Glu Gly Asn Leu Val Pro	
585 590 595	
aat atc ttg tgg ggg aat gct gta gat gtc aga tcc tta atg cag gtt	1939
Asn Ile Leu Trp Gly Asn Ala Val Asp Val Arg Ser Leu Met Gln Val	
600 605 610	
caa gag acc cat gca tcg agc tta cag aca gat cga ggg ctg tgg atc	1987
Gln Glu Thr His Ala Ser Ser Leu Gln Thr Asp Arg Gly Leu Trp Ile	
615 620 625	
gat gga att ggg aat ttc ttc cat gta tct gcc tcc gaa gac aat ata	2035
Asp Gly Ile Gly Asn Phe Phe His Val Ser Ala Ser Glu Asp Asn Ile	
630 635 640 645	
agg tac cgt cat aac agc ggt gga tat gtt cta tct gta aat aat gag	2083
Arg Tyr Arg His Asn Ser Gly Gly Tyr Val Leu Ser Val Asn Asn Glu	
650 655 660	
atc aca cct aag cac tat act tcg atg gca ttt tcc caa ctc ttt agt	2131
Ile Thr Pro Lys His Tyr Thr Ser Met Ala Phe Ser Gln Leu Phe Ser	
665 670 675	
aga gac aag gac tat gcg gtt tcc aac aac gaa tac aga atg tat tta	2179
Arg Asp Lys Asp Tyr Ala Val Ser Asn Asn Glu Tyr Arg Met Tyr Leu	
680 685 690	
gga tcg tat ctc tat caa tat aca acc tcc cta ggg aat att ttc cgt	2227
Gly Ser Tyr Leu Tyr Gln Tyr Thr Thr Ser Leu Gly Asn Ile Phe Arg	
695 700 705	
tat gct tcg cgt aac cct aat gta aac gtc ggg att ctc tca aga agg	2275
Tyr Ala Ser Arg Asn Pro Asn Val Asn Val Gly Ile Leu Ser Arg Arg	
710 715 720 725	
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Phe Leu Gln Asn Pro Leu Met Ile Phe His Phe Leu Cys Ala Tyr Gly	
730 735 740	
cat gcc acc aat gat atg aaa aca gac tac gca aat ttc cct atg gtg	2371
His Ala Thr Asn Asp Met Lys Thr Asp Tyr Ala Asn Phe Pro Met Val	
745 750 755	
aaa aac agc tgg aga aac aat tgt tgg gct ata gag tgc gga ggg agc	2419
Lys Asn Ser Trp Arg Asn Asn Cys Trp Ala Ile Glu Cys Gly Gly Ser	
760 765 770	
atg cct cta ttg gta ttt gag aac gga aga ctt ttc caa ggt gcc atc	2467
Met Pro Leu Val Phe Glu Asn Gly Arg Leu Phe Gln Gly Ala Ile	
775 780 785	

15/55

cca ttt atg aaa cta caa tta gtt tat gct tat cat gga gat ttc aaa 2515  
 Pro Phe Met Lys Leu Gln Leu Val Tyr Ala Tyr His Gly Asp Phe Lys  
 790 795 800 805

gag acg act gca gat ggc cgt aga ttt agt aat ggg agt tta aca tcg 2563  
 Glu Thr Thr Ala Asp Gly Arg Arg Phe Ser Asn Gly Ser Leu Thr Ser  
 810 815 820

att tct gta cct cta ggc ata cgc ttt gag aag ctg gca ctt tct cag 2611  
 Ile Ser Val Pro Leu Gly Ile Arg Phe Glu Lys Leu Ala Leu Ser Gln  
 825 830 835

gat gta ctc tat gac ttt agt ttc tcc tat att cct gat att ttc cgt 2659  
 Asp Val Leu Tyr Asp Phe Ser Phe Ser Tyr Ile Pro Asp Ile Phe Arg  
 840 845 850

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 Lys Asp Pro Ser Cys Glu Ala Ala Leu Val Ile Ser Gly Asp Ser Trp  
 855 860 865

ctt gtt ccg gca gca cac gta tca aga cat gct ttt gta ggg agt gga 2755  
 Leu Val Pro Ala Ala His Val Ser Arg His Ala Phe Val Gly Ser Gly  
 870 875 880 885

acg ggt cgg tat cac ttt aac gac tat act gag ctc tta tgt cga gga 2803  
 Thr Gly Arg Tyr His Phe Asn Asp Tyr Thr Glu Leu Leu Cys Arg Gly  
 890 895 900

agt ata gaa tgc cgc ccc cat gct agg aat tat aat ata aac tgt gga 2851  
 Ser Ile Glu Cys Arg Pro His Ala Arg Asn Tyr Asn Ile Asn Cys Gly  
 905 910 915

agc aaa ttt cgt ttt tagaagggtt ccattgcttg tgtggttccg gatcttaact 2906  
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 Met Pro Ser Ser Trp  
 1 5

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aaa agg tta tta cag gtt ctg tct cac aaa ata gca gct aca gaa agt 163  
 Lys Arg Leu Leu Gln Val Leu Ser His Lys Ile Ala Ala Thr Glu Ser  
                   10                  15                  20

ggt ggg ggt atc tac gct aag gat att caa cta caa gct cta cct gga 211  
 Gly Gly Gly Ile Tyr Ala Lys Asp Ile Gln Leu Gln Ala Leu Pro Gly  
                   25                  30                  35

agc ttc aca att acc gat aat aaa gtc gaa act agt ctt act act agc 259  
 Ser Phe Thr Ile Thr Asp Asn Lys Val Glu Thr Ser Leu Thr Thr Ser  
                   40                  45                  50

act aat tta tat ggt ggg ggc atc tat tcc agt gga gct gtc acg cta 307  
 Thr Asn Leu Tyr Gly Gly Gly Ile Tyr Ser Ser Gly Ala Val Thr Leu  
                   55                  60                  65

acc aat ata tct gga acc ttt ggc att aca gga aac tct gtt atc aat 355  
 Thr Asn Ile Ser Gly Thr Phe Gly Ile Thr Gly Asn Ser Val Ile Asn  
                   70                  75                  80                  85

aca gcg aca tcc cag gat gca gat ata caa ggt ggg ggc att tat gca 403  
 Thr Ala Thr Ser Gln Asp Ala Asp Ile Gln Gly Gly Gly Ile Tyr Ala  
                   90                  95                  100

acc acg tct ctc tca ata aat caa tgt aat aca ccc att cta ttt agc 451  
 Thr Thr Ser Leu Ser Ile Asn Gln Cys Asn Thr Pro Ile Leu Phe Ser  
                   105                  110                  115

aac aac tct gct gcc act aaa aaa aca tca aca aca aag caa att gct 499  
 Asn Asn Ser Ala Ala Thr Lys Lys Thr Ser Thr Thr Lys Gln Ile Ala  
                   120                  125                  130

ggt ggg gct atc ttc tcc gct gca gta act atc gag aat aac tct cag 547  
 Gly Gly Ala Ile Phe Ser Ala Ala Val Thr Ile Glu Asn Asn Ser Gln  
                   135                  140                  145

ccc att att ttc tta aat aat tcc gca aag tcg gaa gca act aca gca 595  
 Pro Ile Ile Phe Leu Asn Asn Ser Ala Lys Ser Glu Ala Thr Thr Ala  
                   150                  155                  160                  165

gca act gca gga aat aaa gat agc tgt gga gga gcc att gca gct aac 643  
 Ala Thr Ala Gly Asn Lys Asp Ser Cys Gly Gly Ala Ile Ala Ala Asn  
                   170                  175                  180

tct gtt act tta aca aat aac cct gaa ata acc ttt aaa gga aat tat 691  
 Ser Val Thr Leu Thr Asn Asn Pro Glu Ile Thr Phe Lys Gly Asn Tyr  
                   185                  190                  195

gca gaa act gga gga gcg att ggc tgt att gat ctt act aat ggc tca 739  
 Ala Glu Thr Gly Gly Ala Ile Gly Cys Ile Asp Leu Thr Asn Gly Ser  
                   200                  205                  210

cct ccc cgt aaa gtc tct att gca gac aac ggt tct gtc ctt ttt caa 787  
 Pro Pro Arg Lys Val Ser Ile Ala Asp Asn Gly Ser Val Leu Phe Gln  
                   215                  220                  225



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gac aac tct gcg tta aat cgc gga ggc gct atc tat gga gag act atc 835  
 Asp Asn Ser Ala Leu Asn Arg Gly Gly Ala Ile Tyr Gly Glu Thr Ile  
 230 235 240 245

gat atc tcc agg aca ggt gcg act ttc atc ggt aac tct tca aaa cat 883  
 Asp Ile Ser Arg Thr Gly Ala Thr Phe Ile Gly Asn Ser Ser Lys His  
 250 255 260

gat gga agt gca att tgc tgt tca aca gcc cta act ctt gcg cca aac 931  
 Asp Gly Ser Ala Ile Cys Cys Ser Thr Ala Leu Thr Leu Ala Pro Asn  
 265 270 275

tcc caa ctt atc ttt gaa aac aat aag gtt acg gaa acc aca gcc act 979  
 Ser Gln Leu Ile Phe Glu Asn Asn Lys Val Thr Glu Thr Thr Ala Thr  
 280 285 290

aca aaa gct tcc ata aat aat tta gga gct gca att tat gga aat aat 1027  
 Thr Lys Ala Ser Ile Asn Asn Leu Gly Ala Ala Ile Tyr Gly Asn Asn  
 295 300 305

gag act agt gac gtc act atc tct tta tca gct gag aat gga agt att 1075  
 Glu Thr Ser Asp Val Thr Ile Ser Leu Ser Ala Glu Asn Gly Ser Ile  
 310 315 320 325

ttc ttt aaa aac aat cta tgc aca gca aca aac aaa tac tgc agt att 1123  
 Phe Phe Lys Asn Asn Leu Cys Thr Ala Thr Asn Lys Tyr Cys Ser Ile  
 330 335 340

gct gga aac gta aaa ttt aca gca ata gaa gct tca gca ggg aaa gct 1171  
 Ala Gly Asn Val Lys Phe Thr Ala Ile Glu Ala Ser Ala Gly Lys Ala  
 345 350 355

ata tct ttc tat gat gca gtt aac gtt cca cca aag aaa caa ttg ctc 1219  
 Ile Ser Phe Tyr Asp Ala Val Asn Val Pro Pro Lys Lys Gln Leu Leu  
 360 365 370

aag agc taaattaaat gaaaaagcga caagtacang gacgtttcta ntttctgggg 1275  
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 <213> Chlamydia pneumoniae

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 <222> (101).. (2713)

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cct Pro	tg Trp	cta Leu	ctt Leu	acc Thr 10	tct Ser	tcg Ser	gct Ala	tta Leu	gtt Val 15	ttc Phe	tcc Ser	cta Leu	cat His	cca Pro 20	cta Leu	163
atg Met	gct Ala	gct Ala	aac Asn 25	acg Thr	gat Asp	ctc Leu	tca Ser	tca Ser 30	tcc Ser	gat Asp	aac Asn	tat Tyr	gaa Glu 35	aat Asn	ggt Gly	211
agt Ser	agt Ser	ggt Gly 40	agc Ser	gca Ala	gca Ala	ttc Phe	act Thr 45	gcc Ala	aag Lys	gaa Glu	act Thr 50	tcg Ser	gat Asp	gct Ala	tca Ser	259
gga Gly	act Thr 55	acc Thr	tac Tyr	act Thr	ctc Leu	act Thr 60	agc Ser	gat Asp	gtt Val	tct Ser	att Ile 65	acg Thr	aat Asn	gta Val	tct Ser	307
gca Ala 70	att Ile	act Thr	cct Pro	gca Ala	gat Asp 75	aaa Lys	agc Ser	tgt Cys	ttt Phe	aca Thr 80	aac Asn	aca Thr	gga Gly	gga Gly	gca Ala 85	355
ttg Leu	agt Ser	ttt Phe	gtt Val 90	gga Gly	gct Ala	gat Asp	cac His	tca Ser	ttg Leu 95	gtt Val	ctg Leu	caa Gln	acc Thr	ata Ile 100	gcg Ala	403
ctt Leu	acg Thr	cat His	gat Asp 105	ggt Gly	gct Ala	gca Ala	att Ile	aac Asn 110	aat Asn	acc Thr	aac Asn	aca Thr	gct Ala 115	ctt Leu	tct Ser	451
ttc Phe	tca Ser	gga Gly 120	ttc Phe	tcg Ser	tca Ser	ctc Leu	tta Leu 125	atc Ile	gac Asp	tca Ser	gct Ala	cca Pro 130	gca Ala	aca Thr	gga Gly	499
act Thr	tcg Ser 135	ggc Gly	ggc Gly	aag Lys	ggt Gly	gct Ala 140	att Ile	tgt Cys	gtg Val	aca Thr	aat Asn 145	aca Thr	gag Glu	gga Gly	ggt Gly	547
act Thr 150	gcg Ala	act Thr	ttt Phe	act Thr	gac Asp 155	aat Asn	gcc Ala	agt Ser	gtc Val	acc Thr 160	ctc Leu	caa Gln	aaa Lys	aat Asn	act Thr 165	595
tca Ser	gaa Glu	aaa Lys	gat Asp	gga Gly 170	gct Ala	gca Ala	gtt Val	tct Ser	gcc Ala 175	tac Tyr	agc Ser	atc Ile	gat Asp	ctt Leu 180	gct Ala	643
aag Lys	act Thr	acg Thr	aca Thr 185	gca Ala	gct Ala	ctc Leu	tta Leu 190	gat Asp	caa Gln	aat Asn	act Thr	agc Ser	aca Thr	aaa Lys	aat Asn	691
ggc Gly	ggg Gly	gcc Ala 200	ctc Leu	tgt Cys	agt Ser	aca Thr	gca Ala 205	aac Asn	act Thr	aca Thr	gtc Val	caa Gln 210	gga Gly	aac Asn	tca Ser	739

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gga acg gtg acc ttc tcc tca aat act gct aca gat aaa ggt ggg ggg	787
Gly Thr Val Thr Phe Ser Ser Asn Thr Ala Thr Asp Lys Gly Gly Gly	
215 220 225	
atc tac tca aaa gaa aag gat agc acg cta gat gcc aat aca gga gtc	835
Ile Tyr Ser Lys Glu Lys Asp Ser Thr Leu Asp Ala Asn Thr Gly Val	
230 235 240 245	
gtt acc ttc aaa tct aat act gca aag acg ggg ggt gct tgg agc tct	883
Val Thr Phe Lys Ser Asn Thr Ala Lys Thr Gly Gly Ala Trp Ser Ser	
250 255 260	
gat gac aat ctt gct ctt acc ggc aac act caa gta ctt ttt cag gaa	931
Asp Asp Asn Leu Ala Leu Thr Gly Asn Thr Gln Val Leu Phe Gln Glu	
265 270 275	
aat aaa aca acc ggc tca gca gca cag gca aat aac ccg gaa ggt tgt	979
Asn Lys Thr Thr Gly Ser Ala Ala Gln Ala Asn Asn Pro Glu Gly Cys	
280 285 290	
ggg gga gca atc tgt tgt tat ctt gct aca gca aca gac aaa act gga	1027
Gly Gly Ala Ile Cys Cys Tyr Leu Ala Thr Ala Thr Asp Lys Thr Gly	
295 300 305	
tta gcc att tct cag aat caa gaa atg agc ttc act agt aat aca aca	1075
Leu Ala Ile Ser Gln Asn Gln Glu Met Ser Phe Thr Ser Asn Thr Thr	
310 315 320 325	
act gcg aat ggt gga gcg atc tac gct act aaa tgt act ctg gat gga	1123
Thr Ala Asn Gly Gly Ala Ile Tyr Ala Thr Lys Cys Thr Leu Asp Gly	
330 335 340	
aac aca act ctt acc ttc gat cag aat act gcg aca gca gga tgt ggc	1171
Asn Thr Thr Leu Thr Phe Asp Gln Asn Thr Ala Thr Ala Gly Cys Gly	
345 350 355	
gga gct atc tat aca gaa act gaa gat ttt tct ctt aag gga agt acg	1219
Gly Ala Ile Tyr Thr Glu Thr Glu Asp Phe Ser Leu Lys Gly Ser Thr	
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gga acc gtg acc ttc agc aca aat aca gca aag aca ggc ggc gcc tta	1267
Gly Thr Val Thr Phe Ser Thr Asn Thr Ala Lys Thr Gly Gly Ala Leu	
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Tyr Ser Lys Gly Asn Ser Ser Leu Thr Gly Asn Thr Asn Leu Leu Phe	
390 395 400 405	
tca ggg aac aaa gct acg ggc ccg agt aat tct tca gca aat caa gag	1363
Ser Gly Asn Lys Ala Thr Gly Pro Ser Asn Ser Ser Ala Asn Gln Glu	
410 415 420	
ggg tgc ggt ggg gca atc cta gcc ttt att gat tca gga tcc gta agc	1411
Gly Cys Gly Gly Ala Ile Leu Ala Phe Ile Asp Ser Gly Ser Val Ser	
425 430 435	

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gat aaa aca gga cta tcg att gca aac aac caa gaa gtc agc ctc act	1459
Asp Lys Thr Gly Leu Ser Ile Ala Asn Asn Gln Glu Val Ser Leu Thr	
440 445 450	
agt aat gct gca aca gta agt ggt ggt gcg atc tat gct acc aaa tgt	1507
Ser Asn Ala Ala Thr Val Ser Gly Gly Ala Ile Tyr Ala Thr Lys Cys	
455 460 465	
act cta act gga aac ggc tcc ctg acc ttt gac ggc aat act gct gga	1555
Thr Leu Thr Gly Asn Gly Ser Leu Thr Phe Asp Gly Asn Thr Ala Gly	
470 475 480 485	
act tca gga ggg gcg atc tat aca gaa act gaa gat ttt act ctt aca	1603
Thr Ser Gly Gly Ala Ile Tyr Thr Glu Thr Glu Asp Phe Thr Leu Thr	
490 495 500	
gga agt aca gga acc gtg acc ttc agc aca aat aca gca aag aca ggc	1651
Gly Ser Thr Gly Thr Val Thr Phe Ser Thr Asn Thr Ala Lys Thr Gly	
505 510 515	
ggc gcc tta tat tct aaa ggc aac aac tct ctg tct ggt aat acc aac	1699
Gly Ala Leu Tyr Ser Lys Gly Asn Asn Ser Leu Ser Gly Asn Thr Asn	
520 525 530	
ctg ctc ttt tca ggg aac aaa gct acg ggc ccg agt aat tct tca gca	1747
Leu Leu Phe Ser Gly Asn Lys Ala Thr Gly Pro Ser Asn Ser Ser Ala	
535 540 545	
aat caa gag ggt tgc ggt ggg gca atc cta tcg ttt ctt gag tca gca	1795
Asn Gln Glu Gly Cys Gly Gly Ala Ile Leu Ser Phe Leu Glu Ser Ala	
550 555 560 565	
tct gta agt act aaa aaa gga ctc tgg att gaa gat aac gaa aac gtg	1843
Ser Val Ser Thr Lys Lys Gly Leu Trp Ile Glu Asp Asn Glu Asn Val	
570 575 580	
agt ctc tct ggt aat act gca aca gta agt ggc ggt gcg atc tat gcg	1891
Ser Leu Ser Gly Asn Thr Ala Thr Val Ser Gly Gly Ala Ile Tyr Ala	
585 590 595	
acc aag tgt gct ctg cat gga aac acg act ctt acc ttt gat ggc aat	1939
Thr Lys Cys Ala Leu His Gly Asn Thr Thr Leu Thr Phe Asp Gly Asn	
600 605 610	
act gcc gaa act gca gga gga gcg atc tat aca gaa acc gaa gat ttt	1987
Thr Ala Glu Thr Ala Gly Gly Ala Ile Tyr Thr Glu Thr Glu Asp Phe	
615 620 625	
act ctt acg gga agt acg gga acc gtg acc ttc agc aca aat aca gca	2035
Thr Leu Thr Gly Ser Thr Gly Thr Val Thr Phe Ser Thr Asn Thr Ala	
630 635 640 645	
aag aca gca ggg gct cta cat act aaa gga aat act tcc ttt acc aaa	2083
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**SUBSTITUTE SHEET (RULE 26)**

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<213> Chlamydia pneumoniae
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Met Thr Asn Ser Ile  
1 5

ttc ata tca aag ttt gga tgt tta tgc gac cca ttt gtc tca gca ttt 163  
Phe Ile Ser Lys Phe Gly Cys Leu Cys Asp Pro Phe Val Ser Ala Phe  
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tat	ccc	act	gcg	cta	tgt	tgt	tcc	tta	tca	gga	aat	gaa	gtc	cct	aac	211
Tyr	Pro	Thr	Ala	Leu	Cys	Cys	Ser	Leu	Ser	Gly	Asn	Glu	Val	Pro	Asn	
			25					30					35			

ctc gcc tct tgt cag atg tct aga aaa gac atc tct gct ttc cac acg 259  
Leu Ala Ser Cys Gln Met Ser Arg Lys Asp Ile Ser Ala Phe His Thr  
40 45 50

tct cca agc ttc cgt ctg aat gta act cca gag ccc ttg gtt tcc tcc 307  
Ser Pro Ser Phe Arg Leu Asn Val Thr Pro Glu Pro Leu Val Ser Ser  
55 60 65

t t t	c g t	c c c	t c t	a a t	c t t	c t t	a a t	g g a	t t c	g g t	c a c	g a t	a t a	a c c	c a g	355
Phe	Arg	Pro	Ser	Asn	Leu	Leu	Asn	Gly	Phe	Gly	His	Asp	Ile	Thr	Gln	
70					75					80					85	

gac atc aca att aca gga aac tct atc aat tct gtt ata gat tat aac 403  
Asp Ile Thr Ile Thr Gly Asn Ser Ile Asn Ser Val Ile Asp Tyr Asn  
90 95 100

tac	cac	tac	gag	gat	gga	ggc	att	ctt	gca	tgt	aaa	aat	ttg	ttc	att	451
Tyr	His	Tyr	Glu	Asp	Gly	Gly	Ile	Leu	Ala	Cys	Lys	Asn	Leu	Phe	Ile	
			105					110					115			

tct gaa aat aaa gga aac tta agt ttt gaa agg aat agc tcc cac agt 499  
Ser Glu Asn Lys Gly Asn Leu Ser Phe Glu Arg Asn Ser Ser His Ser  
120 125 130

tct	gga	ggg	gct	ctc	tac	agt	gtt	cgg	gaa	tgc	tgg	att	tct	aag	aat	547
Ser	Gly	Gly	Ala	Leu	Tyr	Ser	Val	Arg	Glu	Cys	Trp	Ile	Ser	Lys	Asn	
	135					140					145					

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cag aac tac tcg ttt att tca aat gcg gct tcc tta gct act act aca	595
Gln Asn Tyr Ser Phe Ile Ser Asn Ala Ala Ser Leu Ala Thr Thr Thr	
150 155 160 165	
act tca gga ttt ggt ggg gct ata cat gca cta gat agc tat att aca	643
Thr Ser Gly Phe Gly Gly Ala Ile His Ala Leu Asp Ser Tyr Ile Thr	
170 175 180	
aat aac tta gga gaa gga caa ttc tta gat aat gtc tct aaa aat aga	691
Asn Asn Leu Gly Glu Gly Gln Phe Leu Asp Asn Val Ser Lys Asn Arg	
185 190 195	
gga gga gct atc tat gtt ggg gtg agt tta tca atc aca gac aac tta	739
Gly Gly Ala Ile Tyr Val Gly Val Ser Leu Ser Ile Thr Asp Asn Leu	
200 205 210	
ggt cct atc gtt atc aag aaa aat caa aca tta gaa gat tcc agc ttt	787
Gly Pro Ile Val Ile Lys Lys Asn Gln Thr Leu Glu Asp Ser Ser Phe	
215 220 225	
gga gga ggc atc ttc tgc aga gcc gta aat ata gaa agg aat tat caa	835
Gly Gly Gly Ile Phe Cys Arg Ala Val Asn Ile Glu Arg Asn Tyr Gln	
230 235 240 245	
aac atc caa atc aat gat aat gct tca gga caa ggg gtg gta tat ttt	883
Asn Ile Gln Ile Asn Asp Asn Ala Ser Gly Gln Gly Val Val Tyr Phe	
250 255 260	
ctg ccc cta gga gtc att atc tct tca aat aaa gaa att ata gag atc	931
Leu Pro Leu Gly Val Ile Ile Ser Ser Asn Lys Glu Ile Ile Glu Ile	
265 270 275	
agc aat cac tcc gca tcc tca att aac aca gca tca gga aaa cta tat	979
Ser Asn His Ser Ala Ser Ser Ile Asn Thr Ala Ser Gly Lys Leu Tyr	
280 285 290	
ccc ggt ggt ggc ggt atc atg tgt acc tcc ctt agt cat gag aac aat	1027
Pro Gly Gly Gly Ile Met Cys Thr Ser Leu Ser His Glu Asn Asn	
295 300 305	
ccc aaa ggt ctt atc ttt aac aat aaa acg gca gca ctt agc ggc gga	1075
Pro Lys Gly Leu Ile Phe Asn Asn Lys Thr Ala Ala Leu Ser Gly Gly	
310 315 320 325	
gta tac aca cga gat ctt tca tct tcc aaa ata acg gtc cgc aca gca	1123
Val Tyr Thr Arg Asp Leu Ser Ser Ser Lys Ile Thr Val Arg Thr Ala	
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Phe Ile Asn Asn Ser Ala Thr Ser Gly Gly Ala Leu Ile Asn Leu Ser	
345 350 355	
ggt ata gga agt act cct caa aat ttc ttc ctc tct gca gac tac ggc	1219
Gly Ile Gly Ser Thr Pro Gln Asn Phe Phe Leu Ser Ala Asp Tyr Gly	
360 365 370	

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gat att cta ttt aac aat aat aca atc aca tct tct tct cct caa ccc	1267
Asp Ile Leu Phe Asn Asn Asn Thr Ile Thr Ser Ser Ser Pro Gln Pro	
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gga tat aga aat gca ctc tat gct gct ccg ggg att aac tta aaa cta	1315
Gly Tyr Arg Asn Ala Leu Tyr Ala Ala Pro Gly Ile Asn Leu Lys Leu	
390 395 400 405	
gga gca aga cag ggt tat aaa att ctc ttt tat gat cct ata gat cac	1363
Gly Ala Arg Gln Gly Tyr Lys Ile Leu Phe Tyr Asp Pro Ile Asp His	
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gat cag acg aca aca gat cct ata gta ttt aat tat gaa ccc cat cac	1411
Asp Gln Thr Thr Thr Asp Pro Ile Val Phe Asn Tyr Glu Pro His His	
425 430 435	
ctt ggc acc gtg ttg ttt tcc gga atc aat gta gat tct aac gca aca	1459
Leu Gly Thr Val Leu Phe Ser Gly Ile Asn Val Asp Ser Asn Ala Thr	
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Asn Pro Leu Asn Phe Leu Ser Lys Phe Ser Asn Ser Ser Arg Leu Glu	
455 460 465	
agg ggt gtg ctc gct att gaa gat cgg gct gct att tct tgc aaa acc	1555
Arg Gly Val Leu Ala Ile Glu Asp Arg Ala Ala Ile Ser Cys Lys Thr	
470 475 480 485	
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Leu Ser Gln Thr Gly Gly Ile Leu Arg Leu Gly Asn Ala Ala Leu Ile	
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Arg Thr Lys Gly Pro Gly Ser Ser Ile Asn Phe Asn Ala Ile Ala Ile	
505 510 515	
aat ctt cct tct att tta caa tca gaa gcc tca gct cca aag ttc tgg	1699
Asn Leu Pro Ser Ile Leu Gln Ser Glu Ala Ser Ala Pro Lys Phe Trp	
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Ile Tyr Pro Thr Leu Thr Gly Ser Thr Tyr Ser Glu Asp Thr Ser Ser	
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Thr Ile Thr Leu Ser Gly Pro Leu Thr Phe Leu Asn Asp Glu Asn Glu	
550 555 560 565	
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Asn Pro Tyr Asp Ser Leu Asp Leu Ser Glu Pro Arg Lys Asp Ile Pro	
570 575 580	
cct cct cta cct cct cga tgt gac tgc aaa aaa atc gat act tcg aat	1891
Pro Pro Leu Pro Pro Arg Cys Asp Cys Lys Lys Ile Asp Thr Ser Asn	
585 590 595	



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ctc att gta gaa gcc atg aac tta gat gag cac tat gga tat cag gga 1939  
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atc tgg tct ccc tat tgg atg gaa act acg act aca aca agc tct aca 1987  
 Ile Trp Ser Pro Tyr Trp Met Glu Thr Thr Thr Thr Thr Ser Ser Thr  
 615 620 625

gta ccg gaa cag acc aat aca aac cac agg cag ctc tac gta gac tgg 2035  
 Val Pro Glu Gln Thr Asn Thr Asn His Arg Gln Leu Tyr Val Asp Trp  
 630 635 640 645

act cct gta gga tac cgc cct aac ccg gaa cgt cac gga gaa ttt att 2083  
 Thr Pro Val Gly Tyr Arg Pro Asn Pro Glu Arg His Gly Glu Phe Ile  
 650 655 660

gct aat acc tta tgg cag tct gcc tat aac gct ctg tta gga atc cgc 2131  
 Ala Asn Thr Leu Trp Gln Ser Ala Tyr Asn Ala Leu Leu Gly Ile Arg  
 665 670 675

atc tta cct cca caa aac ctc aaa gag cat gac ctt gaa gcc tct ctg 2179  
 Ile Leu Pro Pro Gln Asn Leu Lys Glu His Asp Leu Glu Ala Ser Leu  
 680 685 690

caa gga ctc ggg ctt cta att aac caa cat aat cgc gag gga cgc aaa 2227  
 Gln Gly Leu Gly Leu Leu Ile Asn Gln His Asn Arg Glu Gly Arg Lys  
 695 700 705

ggc ttc cga aac cat act acg ggc tat gca gca aca acc tca gca aaa 2275  
 Gly Phe Arg Asn His Thr Thr Gly Tyr Ala Ala Thr Thr Ser Ala Lys  
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act gca gca cga cat agt ttc tct tta gga ttc gca caa atg ttc tcc 2323  
 Thr Ala Ala Arg His Ser Phe Ser Leu Gly Phe Ala Gln Met Phe Ser  
 730 735 740

aaa act aga gaa cgt caa tct cca agt acg act tcc tcc cac aac tac 2371  
 Lys Thr Arg Glu Arg Gln Ser Pro Ser Thr Thr Ser Ser His Asn Tyr  
 745 750 755

ttt gca gga ctc cgc ttc gac agt ctc ctc ttc agg gac ttc atc tct 2419  
 Phe Ala Gly Leu Arg Phe Asp Ser Leu Leu Phe Arg Asp Phe Ile Ser  
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aca ggg cta tcc cta ggt tat agc tac gga gat cac cat atg ctt tgc 2467  
 Thr Gly Leu Ser Leu Gly Tyr Ser Tyr Gly Asp His His Met Leu Cys  
 775 780 785

cac tat aca gaa atc tta aaa ggg tcg tcc aaa gcc ttc ttt aat aac 2515  
 His Tyr Thr Glu Ile Leu Lys Gly Ser Ser Lys Ala Phe Phe Asn Asn  
 790 795 800 805

cac act ttg gta gcc tct cta gac tgc aca ttc tta cca gct aga atc 2563  
 His Thr Leu Val Ala Ser Leu Asp Cys Thr Phe Leu Pro Ala Arg Ile  
 810 815 820

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acc cgc act ctc gaa ctc cag ccc ttt atc agt gcc att gct ctg cgc 2611  
 Thr Arg Thr Leu Glu Leu Gln Pro Phe Ile Ser Ala Ile Ala Leu Arg  
                   825                                  830                                  835

tgt tcc cag gcc tcg ttc caa gaa act gga gac cat ata aga aaa ttc 2659  
 Cys Ser Gln Ala Ser Phe Gln Glu Thr Gly Asp His Ile Arg Lys Phe  
                   840                                  845                                  850

cat cca aaa cat ccc ctt aca gat ctt tcc tct ccc ata ggc ttc cgt 2707  
 His Pro Lys His Pro Leu Thr Asp Leu Ser Ser Pro Ile Gly Phe Arg  
                   855                                  860                                  865

tct gaa tgg aaa act tca cat cat atc ccc atg cta tgg act acg gaa 2755  
 Ser Glu Trp Lys Thr Ser His His Ile Pro Met Leu Trp Thr Thr Glu  
                   870                                  875                                  880                                  885

ata tcc tac gta cct acc cta tac aga aaa aat cca gaa atg ttc acg 2803  
 Ile Ser Tyr Val Pro Thr Leu Tyr Arg Lys Asn Pro Glu Met Phe Thr  
                                   890                                  895                                  900

aca cta ctc atc agc aat gga aca tgg aca aca caa gca act ccc gtc 2851  
 Thr Leu Leu Ile Ser Asn Gly Thr Trp Thr Thr Gln Ala Thr Pro Val  
                                   905                                  910                                  915

tcc tat aat tcc gta gct gca aaa ata aaa aat act tcc caa ctt ttc 2899  
 Ser Tyr Asn Ser Val Ala Ala Lys Ile Lys Asn Thr Ser Gln Leu Phe  
                   920                                  925                                  930

tca aga gta acc tta tcc tta gat tat tca gct caa gtc tcc tcg tca 2947  
 Ser Arg Val Thr Leu Ser Leu Asp Tyr Ser Ala Gln Val Ser Ser Ser  
                   935                                  940                                  945

act gta ggt caa tac ctt aaa gct gag agt cat tgc aca ttt 2989  
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                   950                                  955                                  960

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	Met	Thr	Ile	Leu	Arg	
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Asn Phe Leu Thr Cys Ser Ala Leu Phe Leu Ala Leu Pro Ala Ala Ala						
	10			15	20	
caa gtt gta tat ctt cat gaa agt gat ggt tat aac ggt gct atc aat						211
Gln Val Val Tyr Leu His Glu Ser Asp Gly Tyr Asn Gly Ala Ile Asn						
	25			30	35	
aat aaa agc tta gaa cct aaa att acc tgt tat cca gaa gga act tct						259
Asn Lys Ser Leu Glu Pro Lys Ile Thr Cys Tyr Pro Glu Gly Thr Ser						
	40			45	50	
tac atc ttt cta gat gac gtg agg att tcc aac gtt aag cat gat caa						307
Tyr Ile Phe Leu Asp Asp Val Arg Ile Ser Asn Val Lys His Asp Gln						
	55			60	65	
gaa gat gct ggg gtt ttt ata aat cga tct ggg aat ctt ttt ttc atg						355
Glu Asp Ala Gly Val Phe Ile Asn Arg Ser Gly Asn Leu Phe Phe Met						
	70			75	80	85
ggc aac cgt tgc aac ttc act ttt cac aac ctt atg acc gag ggt ttt						403
Gly Asn Arg Cys Asn Phe Thr Phe His Asn Leu Met Thr Glu Gly Phe						
	90			95	100	
ggc gct gcc att tgc aac cgc gtt gga gac acc act ctc act ctc tct						451
Gly Ala Ala Ile Ser Asn Arg Val Gly Asp Thr Thr Leu Thr Leu Ser						
	105			110	115	
aat ttt tct tac tta gcg ttc acc tca gca cct cta cta cct caa gga						499
Asn Phe Ser Tyr Leu Ala Phe Thr Ser Ala Pro Leu Leu Pro Gln Gly						
	120			125	130	
caa gga gcg att tat agt ctt ggt tcc gtg atg atc gaa aat agt gag						547
Gln Gly Ala Ile Tyr Ser Leu Gly Ser Val Met Ile Glu Asn Ser Glu						
	135			140	145	
gaa gtg act ttc tgt ggg aac tac tct tgc tgg agt gga gct gcg att						595
Glu Val Thr Phe Cys Gly Asn Tyr Ser Ser Trp Ser Gly Ala Ala Ile						
	150			155	160	165
tat act ccc tac ctt tta ggt tct aag gcg agt cgt cct tca gta aat						643
Tyr Thr Pro Tyr Leu Leu Gly Ser Lys Ala Ser Arg Pro Ser Val Asn						
	170			175	180	
ctc agc ggg aac cgc tac ctg gtg ttt aga gac aat gtg agc caa gtt						691
Leu Ser Gly Asn Arg Tyr Leu Val Phe Arg Asp Asn Val Ser Gln Val						
	185			190	195	
tat ggc ggc gcc ata tct acc cac aat ctc aca ctc acg act cga gga						739
Tyr Gly Gly Ala Ile Ser Thr His Asn Leu Thr Leu Thr Arg Gly						
	200			205	210	

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cct tcg tgt ttt gaa aat aat cat gct tat cat gac gtg aat agt aat	787
Pro Ser Cys Phe Glu Asn Asn His Ala Tyr His Asp Val Asn Ser Asn	
215 220 225	
gga gga gcc att gcc att gct cct gga gga tcg atc tct ata tcc gtg	835
Gly Gly Ala Ile Ala Ile Ala Pro Gly Gly Ser Ile Ser Ile Ser Val	
230 235 240 245	
aaa agc gga gat ctc atc ttc aaa gga aat aca gca tca caa gac gga	883
Lys Ser Gly Asp Leu Ile Phe Lys Gly Asn Thr Ala Ser Gln Asp Gly	
250 255 260	
aat aca ata cac aac tcc atc cat ctg caa tct gga gca cag ttt aag	931
Asn Thr Ile His Asn Ser Ile His Leu Gln Ser Gly Ala Gln Phe Lys	
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Asn Leu Arg Ala Val Ser Glu Ser Gly Val Tyr Phe Tyr Asp Pro Ile	
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Glu Gly Lys Glu Thr Tyr Glu Gly Thr Ile Ser Phe Ser Gly Leu Cys	
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Leu Asp Asp His Glu Val Cys Ala Glu Asn Leu Thr Ser Thr Ile Leu	
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caa gat gtc aca tta gca gga gga act ctc tct cta tcg gat ggg gtt	1171
Gln Asp Val Thr Leu Ala Gly Gly Thr Leu Ser Leu Ser Asp Gly Val	
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Thr Leu Gln Leu His Ser Phe Lys Gln Glu Ala Ser Ser Thr Leu Thr	
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Met Ser Pro Gly Thr Thr Leu Leu Cys Ser Gly Asp Ala Arg Val Gln	
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Asn Leu His Ile Leu Ile Glu Asp Thr Asp Asn Phe Val Pro Val Arg	
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att cgc gcc gag gac aag gat gct ctt gtc tca tta gaa aaa ctt aaa	1363
Ile Arg Ala Glu Asp Lys Asp Ala Leu Val Ser Leu Glu Lys Leu Lys	
410 415 420	
gtt gcc ttt gag gct tat tgg tcc gtc tat gac ttt cct caa ttt aag	1411
Val Ala Phe Glu Ala Tyr Trp Ser Val Tyr Asp Phe Pro Gln Phe Lys	
425 430 435	

gaa gcc ttt acg att cct ctt ctt gaa ctt cta ggg cct tct ttt gac	1459
Glu Ala Phe Thr Ile Pro Leu Leu Glu Leu Leu Gly Pro Ser Phe Asp	
440 445 450	
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Ser Leu Leu Leu Gly Glu Thr Thr Leu Glu Arg Thr Gln Val Thr Thr	
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Pro Pro Ser Leu Asp Lys Asp Arg Arg Ile Thr Pro Thr Lys Lys Thr	
490 495 500	
gtt ttc ctc act tgg aat cct gag atc act tct acg cca taatctctaa	1652
Val Phe Leu Thr Trp Asn Pro Glu Ile Thr Ser Thr Pro	
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Met Gly Ile Ser Leu	
1 5	
cca gag ctt ttt tcc aac cta ggt tct gct tac tta gat tat atc ttt	163
Pro Glu Leu Phe Ser Asn Leu Gly Ser Ala Tyr Leu Asp Tyr Ile Phe	
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caa cat cct ccg gcc tat gtt tgg tca gtt ttt ctt ctt tta tta gcc	211
Gln His Pro Pro Ala Tyr Val Trp Ser Val Phe Leu Leu Leu Leu Ala	
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cgt ctg ctt cct att ttt gct gta gct ccc ttc tta gga gca aag ctc	259
Arg Leu Leu Pro Ile Phe Ala Val Ala Pro Phe Leu Gly Ala Lys Leu	
40 45 50	
ttt ccc tcc cct att aaa atc ggg att agt ctc tct tgg ctt gca atc	307
Phe Pro Ser Pro Ile Lys Ile Gly Ile Ser Leu Ser Trp Leu Ala Ile	
55 60 65	

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 Ile Phe Pro Lys Val Leu Ala Asp Thr Gln Ile Thr Asn Tyr Met Asp  
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aac aat ctc ttt tat gtt tta ctt gtg aag gag atg atc ata ggc att 403  
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 His Tyr Phe Val Thr Ile Ile Phe Trp Leu Val Gly Gly His Arg Ile  
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gta atc tct ttg tta ttg caa act ctt gaa gtc att ccg atc cat agt 643  
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ttc ttt cct gcc gag atg atg agc tta agt gcc ccg att tgg att act 691  
 Phe Phe Pro Ala Glu Met Met Ser Leu Ser Ala Pro Ile Trp Ile Thr  
 185 190 195

atg atc aag atg tgc cag ctc tgt ctc gtg atg acc ata cag ctg agt 739  
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gct cct gca gct ttg gcg atg tta atg tcc gac cta ttc tta ggg att 787  
 Ala Pro Ala Ala Leu Ala Met Leu Met Ser Asp Leu Phe Leu Gly Ile  
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 Ile Asn Arg Met Ala Pro Gln Val Gln Val Ile Tyr Leu Leu Ser Ala  
 230 235 240 245

ctt aag gct ttc atg ggt ctt ctc ttt ctc acc ctg gcg tgg tgg ttc 883  
 Leu Lys Ala Phe Met Gly Leu Leu Phe Leu Thr Leu Ala Trp Trp Phe  
 250 255 260

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 Ile Ile Lys Gln Ile Asp Tyr Phe Thr Leu Ala Trp Phe Lys Glu Val  
 265 270 275

ccc att atg ctc cta ggt tcc aac cct caa gta ctc taatcccccta 977  
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 280 285

31/55

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 Met Lys His Ser Lys  
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 Glu Asp Asp Leu Ser Arg Phe Leu Pro Lys Asn Leu Leu Val Glu Ser  
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cct cat ccc gaa gaa atc cct tta aaa tct tta tct ttt acg atg agt 211  
 Pro His Pro Glu Glu Ile Pro Leu Lys Ser Leu Ser Phe Thr Met Ser  
 25 30 35

tgg cta cct aca att cat cct tca tgg att acc att gcc atg aaa gag 259  
 Trp Leu Pro Thr Ile His Pro Ser Trp Ile Thr Ile Ala Met Lys Glu  
 40 45 50

ttc cct cct gaa atc caa ggt caa tta tta gcg tgg ttg cca gag cct 307  
 Phe Pro Pro Glu Ile Gln Gly Gln Leu Leu Ala Trp Leu Pro Glu Pro  
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tta gtt caa gaa att cta ccc tta ctg cct ggc atc tct ata gcc cca 355  
 Leu Val Gln Glu Ile Leu Pro Leu Leu Pro Gly Ile Ser Ile Ala Pro  
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cat cgc tgt gca cct ttc gga gcc ttc tat ctt cta gat atg cta agt 403  
 His Arg Cys Ala Pro Phe Gly Ala Phe Tyr Leu Leu Asp Met Leu Ser  
 90 95 100

aaa aag atc cgt cct tgt gga att aca gaa gaa atc ttt ctt cct gca 451  
 Lys Lys Ile Arg Pro Cys Gly Ile Thr Glu Glu Ile Phe Leu Pro Ala  
 105 110 115

tcc tca gca aat gct ata ctt tac tat aca ggt cct gta aag atc gct 499  
 Ser Ser Ala Asn Ala Ile Leu Tyr Tyr Thr Gly Pro Val Lys Ile Ala  
 120 125 130

32/55

tta atc aac tgc cta ggt ctt tat tct att gct aaa gag ttg aag cac 547  
 Leu Ile Asn Cys Leu Gly Leu Tyr Ser Ile Ala Lys Glu Leu Lys His  
 135 140 145

att ctg gat aag gtt gtg att gaa cga gtg aag aat gct .ctc tcc cct 595  
 Ile Leu Asp Lys Val Val Ile Glu Arg Val Lys Asn Ala Leu Ser Pro  
 150 155 160 165

aca gag aaa ctc ttt ctt acc tac tgc caa tct cat ccg atg aaa cat 643  
 Thr Glu Lys Leu Phe Leu Thr Tyr Cys Gln Ser His Pro Met Lys His  
 170 175 180

tta gaa act acg aat ttt ctt tct tct tgg act act gat gca gaa tta 691  
 Leu Glu Thr Thr Asn Phe Leu Ser Ser Trp Thr Thr Asp Ala Glu Leu  
 185 190 195

cga cag ttc gtt cat aag caa ggg tta gag ttt tta ggt aaa gca tta 739  
 Arg Gln Phe Val His Lys Gln Gly Leu Glu Phe Leu Gly Lys Ala Leu  
 200 205 210

aca aaa gaa aac gct tct ttt cta tgg tat ttt cta cgt agg tta gat 787  
 Thr Lys Glu Asn Ala Ser Phe Leu Trp Tyr Phe Leu Arg Arg Leu Asp  
 215 220 225

gtc ggt cga gca tat atc gtc gag cag act tta aaa aca tgg tat gac 835  
 Val Gly Arg Ala Tyr Ile Val Glu Gln Thr Leu Lys Thr Trp Tyr Asp  
 230 235 240 245

cat ccc tat gtg gat tat ttt aag tcc cgc cta gaa caa tgc atg aaa 883  
 His Pro Tyr Val Asp Tyr Phe Lys Ser Arg Leu Glu Gln Cys Met Lys  
 250 255 260

gtc tta gtg aaa taaaagcttt ataagtaaag atttagcttt atacaaagta 935  
 Val Leu Val Lys  
 265

tagaaaaata acacg 950

<210> 13  
 <211> 500  
 <212> DNA  
 <213> Chlamydia pneumoniae

<220>  
 <221> CDS  
 <222> (101)..(385)

<400> 13  
 cgatttcgtt acctttaaaag ttacttttga tcgtcatggt agacggatgg acattactgc 60

tccaagggct tatgatcagc tttaaataag gacacgtgcc atg tta gca ttt ttc 115  
 Met Leu Ala Phe Phe  
 1 5



33/55

gca act agt ttc aaa tct gtt ctt ttt gag tac tcc tac caa tca tta 163  
Ala Thr Ser Phe Lys Ser Val Leu Phe Glu Tyr Ser Tyr Gln Ser Leu  
10 15 20

tta ctt att ttg att gtt tcg gca cct ccc atc atc tta gct tcc ata 211  
Leu Leu Ile Leu Ile Val Ser Ala Pro Pro Ile Ile Leu Ala Ser Ile  
25 30 35

gtc ggg att atg gtt gcg atc ttc caa gcc gca aca caa atc caa gaa 259  
Val Gly Ile Met Val Ala Ile Phe Gln Ala Ala Thr Gln Ile Gln Glu  
40 45 50

cag acc ttc gct ttt gca gtc aaa cta gtc gtg att ttt gga acc tta 307  
Gln Thr Phe Ala Phe Ala Val Lys Leu Val Val Ile Phe Gly Thr Leu  
55 60 65

atg atc tct gga ggg tgg ctt agc aat atg att tta cgc ttt gca ggt 355  
Met Ile Ser Gly Gly Trp Leu Ser Asn Met Ile Leu Arg Phe Ala Gly  
70 75 80 85

cag att ttc caa aac ttc tat aaa tgg aaa taaagagctt atgggaatct 405  
Gln Ile Phe Gln Asn Phe Tyr Lys Trp Lys  
90 95

ctctaccaga gcttttttcc aacctaggtt ctgcttactt agattatatac tttcaacatc 465

ctccggccta tgtttggtca gtttttcttc tttta 500

<210> 14

<211> 552

<212> PRT

<213> Chlamydia pneumoniae

<400> 14

Met Val Ser Ser Pro Ile Leu Asn Val Pro Leu Lys Asn His Ala Ser  
1 5 10 15

Val Ser Gly Lys Phe Thr His Arg Glu Val Ser Lys Leu Ala Ser Asp  
20 25 30

Leu Lys Ser Gly Ala Met Ser Phe Val Pro Glu Val Leu Ser Glu Glu  
35 40 45

Thr Ile Ser Ser Asp Leu Gly Lys Lys Gln Cys Thr Gln Gly Ile Ile  
50 55 60

Ser Ala Cys Cys Gly Leu Ala Met Leu Ile Val Leu Met Ser Val Tyr  
65 70 75 80

Tyr Arg Phe Gly Gly Val Ile Ala Ser Gly Ala Val Leu Leu Asn Leu  
85 90 95

Leu Leu Ile Trp Ala Ala Leu Gln Tyr Leu Asp Ala Pro Leu Thr Leu  
100 105 110

34/55

Ser Gly Leu Ala Gly Ile Val Leu Ala Met Gly Met Ala Val Asp Ala  
 115 120 125  
 Asn Val Leu Val Phe Glu Arg Ile Arg Glu Glu Phe Leu Leu Ser Gln  
 130 135 140  
 Ser Leu Lys Lys Ser Val Glu Lys Gly Tyr Thr Lys Ala Phe Gly Ala  
 145 150 155 160  
 Ile Phe Asp Ser Asn Leu Thr Thr Val Leu Ala Ser Ala Leu Leu Phe  
 165 170 175  
 Phe Leu Asp Thr Gly Pro Ile Lys Gly Phe Ala Leu Thr Leu Ile Leu  
 180 185 190  
 Gly Ile Phe Ser Ser Met Phe Thr Ala Leu Phe Met Thr Lys Phe Phe  
 195 200 205  
 Phe Met Leu Trp Met Asn Lys Thr Gln His Thr Gln Leu His Met Met  
 210 215 220  
 Asn Lys Phe Val Gly Ile Lys His Asp Phe Leu Arg Gly Cys Lys Lys  
 225 230 235 240  
 Leu Trp Ala Val Ser Gly Ser Val Phe Leu Leu Gly Cys Val Ala Leu  
 245 250 255  
 Gly Phe Gly Ala Trp Asn Ser Val Leu Gly Met Asp Phe Lys Gly Gly  
 260 265 270  
 Tyr Ala Phe Thr Phe Asn Pro Lys Glu His Gly Ile Ser Asp Val Ala  
 275 280 285  
 Gln Met Arg Gly Lys Val Val His Lys Leu Gln Glu Ala Gly Leu Ser  
 290 295 300  
 Ser Arg Asp Phe Arg Ile Gln Thr Phe Gly Ser Ser Glu Lys Ile Lys  
 305 310 315 320  
 Ile Tyr Phe Ser Asp Lys Ala Leu Ser Tyr Thr Lys Gln Ile Arg Ala  
 325 330 335  
 Ser Leu Leu Lys Leu Thr Ile Met Ser Trp Arg Tyr Cys Gly Ile Val  
 340 345 350  
 Val Arg Asn Arg Pro Arg Phe Leu Tyr Gly Asn Ser Lys Arg Asn Ala  
 355 360 365  
 Lys Phe Trp Ser Lys Val Ser Ser Lys Leu Ser Lys Lys Met Arg Tyr  
 370 375 380  
 Gln Ala Thr Ile Gly Leu Leu Gly Ala Leu Ala Ile Ile Leu Leu Tyr  
 385 390 395 400

35/55

Val Ser Leu Arg Phe Glu Trp Gln Tyr Ala Phe Ser Ala Val Cys Ala  
 405 410 415

Leu Ile His Asp Leu Leu Ala Thr Cys Ala Val Leu Phe Ile Ala His  
 420 425 430

Phe Phe Leu Lys Lys Ile Gln Ile Asp Leu Gln Ala Ile Gly Ala Leu  
 435 440 445

Met Thr Val Leu Gly Tyr Ser Leu Asn Asn Thr Leu Ile Ile Phe Asp  
 450 455 460

Arg Ile Arg Glu Asp Arg Gln Ala Asn Leu Phe Thr Pro Met His Val  
 465 470 475 480

Leu Val Asn Asp Ala Leu Gln Lys Thr Phe Ser Arg Thr Val Met Thr  
 485 490 495

Thr Ala Thr Thr Leu Ser Val Leu Leu Met Leu Leu Phe Ile Gly Gly  
 500 505 510

Ser Ser Val Phe Asn Phe Ala Phe Ile Met Thr Ile Gly Ile Leu Leu  
 515 520 525

Gly Thr Leu Ser Ser Leu Tyr Ile Ala Pro Pro Leu Leu Leu Phe Met  
 530 535 540

Val Arg Lys Glu Asn Arg Ser Lys  
 545 550

<210> 15  
 <211> 196  
 <212> PRT  
 <213> Chlamydia pneumoniae

<400> 15  
 Met Ser Ser Asn Leu His Pro Val Gly Gly Thr Gly Thr Gly Ala Ala  
 1 5 10 15

Ala Pro Glu Ser Val Leu Asn Ile Val Glu Glu Ile Ala Ala Ser Gly  
 20 25 30

Ser Val Thr Ala Gly Leu Gln Ala Ile Thr Ser Ser Pro Gly Met Val  
 35 40 45

Asn Leu Leu Ile Gly Trp Ala Lys Thr Lys Phe Ile Gln Pro Ile Arg  
 50 55 60

Glu Ser Lys Leu Phe Gln Ser Arg Ala Cys Gln Ile Thr Leu Leu Val  
 65 70 75 80

Leu Gly Ile Leu Leu Val Val Ala Gly Leu Ala Cys Met Phe Ile Phe  
 85 90 95

36/55

His Ser Gln Leu Gly Ala Asn Ala Phe Trp Leu Ile Ile Pro Ala Ala  
 100 105 110  
 Ile Gly Leu Ile Lys Leu Leu Val Thr Ser Leu Cys Phe Asp Glu Ala  
 115 120 125  
 Cys Thr Ser Glu Lys Leu Met Val Phe Gln Lys Trp Ala Gly Val Leu  
 130 135 140  
 Glu Asp Gln Leu Asp Asp Gly Ile Leu Asn Asn Ser Asn Lys Ile Phe  
 145 150 155 160  
 Gly His Val Lys Thr Glu Gly Asn Thr Ser Arg Ala Thr Thr Pro Val  
 165 170 175  
 Leu Asn Asp Gly Arg Gly Thr Pro Val Leu Ser Pro Leu Val Ser Lys  
 180 185 190  
 Ile Ala Arg Val  
 195  
 <210> 16  
 <211> 245  
 <212> PRT  
 <213> Chlamydia pneumoniae  
 <400> 16  
 Met Thr Ile Arg Ile Leu Ala Glu Gly Leu Ala Phe Arg Tyr Gly Ser  
 1 5 10 15  
 Lys Gly Pro Asn Ile Ile His Asp Val Ser Phe Ser Val Tyr Asp Gly  
 20 25 30  
 Asp Phe Ile Gly Ile Ile Gly Pro Asn Gly Gly Gly Lys Ser Thr Leu  
 35 40 45  
 Thr Met Leu Ile Leu Gly Leu Leu Thr Pro Thr Phe Gly Ser Leu Lys  
 50 55 60  
 Thr Phe Pro Ser His Ser Ala Gly Lys Gln Thr His Ser Met Ile Gly  
 65 70 75 80  
 Trp Val Pro Gln His Phe Ser Tyr Asp Pro Cys Phe Pro Ile Ser Val  
 85 90 95  
 Lys Asp Val Val Leu Ser Gly Arg Leu Ser Gln Leu Ser Trp His Gly  
 100 105 110  
 Lys Tyr Lys Lys Lys Asp Phe Glu Ala Val Asp His Ala Leu Asp Leu  
 115 120 125  
 Val Gly Leu Ser Asp Thr Thr Thr Ala Phe Ala His Leu Ser Gly  
 130 135 140  
 Gly Gln Ile Gln Arg Val Leu Leu Ala Arg Ala Leu Ala Ser Tyr Pro  
 145 150 155 160

37/55

Glu Ile Leu Ile Leu Asp Glu Pro Thr Thr Asn Ile Asp Pro Asp Asn  
 165 170 175

Gln Gln Arg Ile Leu Ser Ile Leu Lys Lys Leu Asn Arg Thr Cys Thr  
 180 185 190

Ile Leu Met Val Thr His Asp Leu His His Thr Thr Asn Tyr Phe Asn  
 195 200 205

Lys Val Phe Tyr Met Asn Lys Thr Leu His Phe Ile Gly Arg His Phe  
 210 215 220

Asp Leu Asn Arg Pro Ile Leu Leu Ser Ser Tyr Lys Asn Gln Glu Phe  
 225 230 235 240

Ser Cys Ser Pro His  
 245

<210> 17  
 <211> 278  
 <212> PRT  
 <213> Chlamydia pneumoniae

<400> 17  
 Met His Lys Val Ile Val Phe Ile Phe Leu Thr Leu Tyr Ser Leu Lys  
 1 5 10 15

Ser Tyr Gly Asn Asp Val Ile Asp Lys Pro His Val Leu Val Ser Ile  
 20 25 30

Ala Pro Tyr Lys Phe Leu Val Glu Gln Ile Ala Glu Glu Thr Cys Phe  
 35 40 45

Val Tyr Ala Ile Val Thr Asn His Tyr Asp Pro His Thr Tyr Glu Leu  
 50 55 60

Pro Pro Gln Gln Ile Lys Glu Leu Arg Gln Gly Asp Leu Trp Phe Arg  
 65 70 75 80

Ile Gly Glu Ala Phe Gly Lys Asn Leu Leu Glu Lys Pro Tyr Met Gln  
 85 90 95

Gln Val Asp Leu Ser Gln Asn Val Ser Leu Ile Gln Gly Lys Pro Cys  
 100 105 110

Cys Asn Gln His Thr Thr Asn Tyr Asp Thr His Thr Trp Leu Ser Pro  
 115 120 125

Lys Asn Leu Lys Val Gln Val Glu Thr Ile Val Thr Thr Leu Ser Lys  
 130 135 140

38/55

Lys Tyr Pro Gln His Ala Thr Leu Tyr Gln Ser Asn Gly Glu Lys Leu  
 145 150 155 160  
 Leu Leu Ala Leu Asp Gln Leu Asn Glu Glu Ile Leu Thr Ile Thr Ser  
 165 170 175  
 Lys Ala Lys Gln Arg His Ile Leu Val Ser His Gly Ala Phe Gly Tyr  
 180 185 190  
 Phe Cys Arg Asp Tyr Asn Phe Ser Gln His Thr Ile Glu Lys Ser Ser  
 195 200 205  
 His Val Glu Pro Ser Pro Lys Asp Val Ala Arg Val Phe Arg Asp Ile  
 210 215 220  
 Glu Gln Tyr Lys Ile Ser Ser Val Ile Leu Leu Glu Tyr Ser Gly Arg  
 225 230 235 240  
 Arg Ser Ser Ala Met Leu Ala Asp Arg Phe His Met His Thr Val Asn  
 245 250 255  
 Leu Asp Pro Tyr Ala Glu Asn Val Leu Val Asn Leu Lys Thr Ile Ala  
 260 265 270  
 Thr Thr Phe Ser Ser Leu  
 275

<210> 18  
 <211> 469  
 <212> PRT  
 <213> Chlamydia pneumoniae

<400> 18  
 Met Gly Pro Gly Ser Val Leu Ser Asn His Ser Lys Glu Ala Gly Gly  
 1 5 10 15  
 Ile Ala Ile Asn Asn Val Ile Ile Asp Phe Ser Glu Ile Val Pro Thr  
 20 25 30  
 Lys Asp Asn Ala Thr Val Ala Pro Pro Thr Leu Lys Leu Val Ser Arg  
 35 40 45  
 Thr Asn Ala Asp Ser Lys Asp Lys Ile Asp Ile Thr Gly Thr Val Thr  
 50 55 60  
 Leu Leu Asp Pro Asn Gly Asn Leu Tyr Gln Asn Ser Tyr Leu Gly Glu  
 65 70 75 80  
 Asp Arg Asp Ile Thr Leu Phe Asn Ile Asp Asn Ser Ala Ser Gly Ala  
 85 90 95  
 Val Thr Ala Thr Asn Val Thr Leu Gln Gly Asn Leu Gly Ala Lys Lys  
 100 105 110

39/55

Gly Tyr Leu Gly Thr Trp Asn Leu Asp Pro Asn Ser Ser Gly Ser Lys  
 115 120 125  
 Ile Ile Leu Lys Trp Thr Phe Asp Lys Tyr Leu Arg Trp Pro Tyr Ile  
 130 135 140  
 Pro Arg Asp Asn His Phe Tyr Ile Asn Ser Ile Trp Gly Ala Gln Asn  
 145 150 155 160  
 Ser Leu Val Thr Val Asn Gln Gly Ile Leu Gly Asn Met Leu Asn Asn  
 165 170 175  
 Ala Arg Phe Glu Asp Pro Ala Phe Asn Asn Phe Trp Ala Ser Ala Ile  
 180 185 190  
 Gly Ser Phe Leu Arg Lys Glu Val Ser Arg Asn Ser Asp Ser Phe Thr  
 195 200 205  
 Tyr His Gly Arg Gly Tyr Thr Ala Ala Val Asp Ala Lys Pro Arg Gln  
 210 215 220  
 Glu Phe Ile Leu Gly Ala Ala Phe Ser Gln Val Phe Gly His Ala Glu  
 225 230 235 240  
 Ser Glu Tyr His Leu Asp Asn Tyr Lys His Lys Gly Ser Gly His Ser  
 245 250 255  
 Thr Gln Ala Ser Leu Tyr Ala Gly Asn Ile Phe Tyr Phe Pro Ala Ile  
 260 265 270  
 Arg Ser Arg Pro Ile Leu Phe Gln Gly Val Ala Thr Tyr Gly Tyr Met  
 275 280 285  
 Gln His Asp Thr Thr Thr Tyr Tyr Pro Ser Ile Glu Glu Lys Asn Met  
 290 295 300  
 Ala Asn Trp Asp Ser Ile Ala Trp Leu Phe Asp Leu Arg Phe Ser Val  
 305 310 315 320  
 Asp Leu Lys Glu Pro Gln Pro His Ser Thr Ala Arg Leu Thr Phe Tyr  
 325 330 335  
 Thr Glu Ala Glu Tyr Thr Arg Ile Arg Gln Glu Lys Phe Thr Glu Leu  
 340 345 350  
 Asp Tyr Asp Pro Arg Ser Phe Ser Ala Cys Ser Tyr Gly Asn Leu Ala  
 355 360 365  
 Ile Pro Thr Gly Phe Ser Val Asp Gly Ala Leu Ala Trp Arg Glu Ile  
 370 375 380  
 Ile Leu Tyr Asn Lys Val Ser Ala Ala Tyr Leu Pro Val Ile Leu Arg  
 385 390 395 400

40/55

Asn Asn Pro Lys Ala Thr Tyr Glu Val Leu Ser Thr Lys Glu Lys Gly  
 405 410 415

Asn Val Val Asn Val Leu Pro Thr Arg Asn Ala Ala Arg Ala Glu Val  
 420 425 430

Ser Ser Gln Ile Tyr Leu Gly Ser Tyr Trp Thr Leu Tyr Gly Thr Tyr  
 435 440 445

Thr Ile Asp Ala Ser Met Asn Thr Leu Val Gln Met Ala Asn Gly Gly  
 450 455 460

Ile Arg Phe Val Phe  
 465

<210> 19

<211> 922

<212> PRT

<213> Chlamydia pneumoniae

<400> 19

Met Arg Phe Ser Leu Cys Gly Phe Pro Leu Val Phe Ser Phe Thr Leu  
 1 5 10 15

Leu Ser Val Phe Asp Thr Ser Leu Ser Ala Thr Thr Ile Ser Leu Thr  
 20 25 30

Pro Glu Asp Ser Phe His Gly Asp Ser Gln Asn Ala Glu Arg Ser Tyr  
 35 40 45

Asn Val Gln Ala Gly Asp Val Tyr Ser Leu Thr Gly Asp Val Ser Ile  
 50 55 60

Ser Asn Val Asp Asn Ser Ala Leu Asn Lys Ala Cys Phe Asn Val Thr  
 65 70 75 80

Ser Gly Ser Val Thr Phe Ala Gly Asn His His Gly Leu Tyr Phe Asn  
 85 90 95

Asn Ile Ser Ser Gly Thr Thr Lys Glu Gly Ala Val Leu Cys Cys Gln  
 100 105 110

Asp Pro Gln Ala Thr Ala Arg Phe Ser Gly Phe Ser Thr Leu Ser Phe  
 115 120 125

Ile Gln Ser Pro Gly Asp Ile Lys Glu Gln Gly Cys Leu Tyr Ser Lys  
 130 135 140

Asn Ala Leu Met Leu Leu Asn Asn Tyr Val Val Arg Phe Glu Gln Asn  
 145 150 155 160

Gln Ser Lys Thr Lys Gly Gly Ala Ile Ser Gly Ala Asn Val Thr Ile  
 165 170 175



41/55

Val Gly Asn Tyr Asp Ser Val Ser Phe Tyr Gln Asn Ala Ala Thr Phe  
 180 185 190  
 Gly Gly Ala Ile His Ser Ser Gly Pro Leu Gln Ile Ala Val Asn Gln  
 195 200 205  
 Ala Glu Ile Arg Phe Ala Gln Asn Thr Ala Lys Asn Gly Ser Gly Gly  
 210 215 220  
 Ala Leu Tyr Ser Asp Gly Asp Ile Asp Ile Asp Gln Asn Ala Tyr Val  
 225 230 235 240  
 Leu Phe Arg Glu Asn Glu Ala Leu Thr Thr Ala Ile Gly Lys Gly Gly  
 245 250 255  
 Ala Val Cys Cys Leu Pro Thr Ser Gly Ser Ser Thr Pro Val Pro Ile  
 260 265 270  
 Val Thr Phe Ser Asp Asn Lys Gln Leu Val Phe Glu Arg Asn His Ser  
 275 280 285  
 Ile Met Gly Gly Gly Ala Ile Tyr Ala Arg Lys Leu Ser Ile Ser Ser  
 290 295 300  
 Gly Gly Pro Thr Leu Phe Ile Asn Asn Ile Ser Tyr Ala Asn Ser Gln  
 305 310 315 320  
 Asn Leu Gly Gly Ala Ile Ala Ile Asp Thr Gly Gly Glu Ile Ser Leu  
 325 330 335  
 Ser Ala Glu Lys Gly Thr Ile Thr Phe Gln Gly Asn Arg Thr Ser Leu  
 340 345 350  
 Pro Phe Leu Asn Gly Ile His Leu Leu Gln Asn Ala Lys Phe Leu Lys  
 355 360 365  
 Leu Gln Ala Arg Asn Gly Tyr Ser Ile Glu Phe Tyr Asp Pro Ile Thr  
 370 375 380  
 Ser Glu Ala Asp Gly Ser Thr Gln Leu Asn Ile Asn Gly Asp Pro Lys  
 385 390 395 400  
 Asn Lys Glu Tyr Thr Gly Thr Ile Leu Phe Ser Gly Glu Lys Ser Leu  
 405 410 415  
 Ala Asn Asp Pro Arg Asp Phe Lys Ser Thr Ile Pro Gln Asn Val Asn  
 420 425 430  
 Leu Ser Ala Gly Tyr Leu Val Ile Lys Glu Gly Ala Glu Val Thr Val  
 435 440 445  
 Ser Lys Phe Thr Gln Ser Pro Gly Ser His Leu Val Leu Asp Leu Gly  
 450 455 460  
 Thr Lys Leu Ile Ala Ser Lys Glu Asp Ile Ala Ile Thr Gly Leu Ala  
 465 470 475 480

42/55

Ile Asp Ile Asp Ser Leu Ser Ser Ser Ser Thr Ala Ala Val Ile Lys  
 485 490 495  
 Ala Asn Thr Ala Asn Lys Gln Ile Ser Val Thr Asp Ser Ile Glu Leu  
 500 505 510  
 Ile Ser Pro Thr Gly Asn Ala Tyr Glu Asp Leu Arg Met Arg Asn Ser  
 515 520 525  
 Gln Thr Phe Pro Leu Leu Ser Leu Glu Pro Gly Ala Gly Gly Ser Val  
 530 535 540  
 Thr Val Thr Ala Gly Asp Phe Leu Pro Val Ser Pro His Tyr Gly Phe  
 545 550 555 560  
 Gln Gly Asn Trp Lys Leu Ala Trp Thr Gly Thr Gly Asn Lys Val Gly  
 565 570 575  
 Glu Phe Phe Trp Asp Lys Ile Asn Tyr Lys Pro Arg Pro Glu Lys Glu  
 580 585 590  
 Gly Asn Leu Val Pro Asn Ile Leu Trp Gly Asn Ala Val Asp Val Arg  
 595 600 605  
 Ser Leu Met Gln Val Gln Glu Thr His Ala Ser Ser Leu Gln Thr Asp  
 610 615 620  
 Arg Gly Leu Trp Ile Asp Gly Ile Gly Asn Phe Phe His Val Ser Ala  
 625 630 635 640  
 Ser Glu Asp Asn Ile Arg Tyr Arg His Asn Ser Gly Gly Tyr Val Leu  
 645 650 655  
 Ser Val Asn Asn Glu Ile Thr Pro Lys His Tyr Thr Ser Met Ala Phe  
 660 665 670  
 Ser Gln Leu Phe Ser Arg Asp Lys Asp Tyr Ala Val Ser Asn Asn Glu  
 675 680 685  
 Tyr Arg Met Tyr Leu Gly Ser Tyr Leu Tyr Gln Tyr Thr Thr Ser Leu  
 690 695 700  
 Gly Asn Ile Phe Arg Tyr Ala Ser Arg Asn Pro Asn Val Asn Val Gly  
 705 710 715 720  
 Ile Leu Ser Arg Arg Phe Leu Gln Asn Pro Leu Met Ile Phe His Phe  
 725 730 735  
 Leu Cys Ala Tyr Gly His Ala Thr Asn Asp Met Lys Thr Asp Tyr Ala  
 740 745 750  
 Asn Phe Pro Met Val Lys Asn Ser Trp Arg Asn Asn Cys Trp Ala Ile  
 755 760 765

[illegible]

Asn Ser Val Ile Asn Thr Ala Thr Ser Gln Asp Ala Asp Ile Gln Gly  
85 90 95

44/55

Gly Gly Ile Tyr Ala Thr Thr Ser Leu Ser Ile Asn Gln Cys Asn Thr  
 100 105 110  
 Pro Ile Leu Phe Ser Asn Asn Ser Ala Ala Thr Lys Lys Thr Ser Thr  
 115 120 125  
 Thr Lys Gln Ile Ala Gly Gly Ala Ile Phe Ser Ala Ala Val Thr Ile  
 130 135 140  
 Glu Asn Asn Ser Gln Pro Ile Ile Phe Leu Asn Asn Ser Ala Lys Ser  
 145 150 155 160  
 Glu Ala Thr Thr Ala Ala Thr Ala Gly Asn Lys Asp Ser Cys Gly Gly  
 165 170 175  
 Ala Ile Ala Ala Asn Ser Val Thr Leu Thr Asn Asn Pro Glu Ile Thr  
 180 185 190  
 Phe Lys Gly Asn Tyr Ala Glu Thr Gly Gly Ala Ile Gly Cys Ile Asp  
 195 200 205  
 Leu Thr Asn Gly Ser Pro Pro Arg Lys Val Ser Ile Ala Asp Asn Gly  
 210 215 220  
 Ser Val Leu Phe Gln Asp Asn Ser Ala Leu Asn Arg Gly Gly Ala Ile  
 225 230 235 240  
 Tyr Gly Glu Thr Ile Asp Ile Ser Arg Thr Gly Ala Thr Phe Ile Gly  
 245 250 255  
 Asn Ser Ser Lys His Asp Gly Ser Ala Ile Cys Cys Ser Thr Ala Leu  
 260 265 270  
 Thr Leu Ala Pro Asn Ser Gln Leu Ile Phe Glu Asn Asn Lys Val Thr  
 275 280 285  
 Glu Thr Thr Ala Thr Thr Lys Ala Ser Ile Asn Asn Leu Gly Ala Ala  
 290 295 300  
 Ile Tyr Gly Asn Asn Glu Thr Ser Asp Val Thr Ile Ser Leu Ser Ala  
 305 310 315 320  
 Glu Asn Gly Ser Ile Phe Phe Lys Asn Asn Leu Cys Thr Ala Thr Asn  
 325 330 335  
 Lys Tyr Cys Ser Ile Ala Gly Asn Val Lys Phe Thr Ala Ile Glu Ala  
 340 345 350  
 Ser Ala Gly Lys Ala Ile Ser Phe Tyr Asp Ala Val Asn Val Pro Pro  
 355 360 365  
 Lys Lys Gln Leu Leu Lys Ser  
 370 375

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&lt;210&gt; 21

&lt;211&gt; 871

&lt;212&gt; PRT

&lt;213&gt; Chlamydia pneumoniae

&lt;400&gt; 21

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Met Lys Tyr Ser Leu Pro Trp Leu Leu Thr Ser Ser Ala Leu Val Phe
  1             5             10             15

Ser Leu His Pro Leu Met Ala Ala Asn Thr Asp Leu Ser Ser Ser Asp
          20             25             30

Asn Tyr Glu Asn Gly Ser Ser Gly Ser Ala Ala Phe Thr Ala Lys Glu
          35             40             45

Thr Ser Asp Ala Ser Gly Thr Thr Tyr Thr Leu Thr Ser Asp Val Ser
          50             55             60

Ile Thr Asn Val Ser Ala Ile Thr Pro Ala Asp Lys Ser Cys Phe Thr
          65             70             75             80

Asn Thr Gly Gly Ala Leu Ser Phe Val Gly Ala Asp His Ser Leu Val
          85             90             95

Leu Gln Thr Ile Ala Leu Thr His Asp Gly Ala Ala Ile Asn Asn Thr
          100            105            110

Asn Thr Ala Leu Ser Phe Ser Gly Phe Ser Ser Leu Leu Ile Asp Ser
          115            120            125

Ala Pro Ala Thr Gly Thr Ser Gly Gly Lys Gly Ala Ile Cys Val Thr
          130            135            140

Asn Thr Glu Gly Gly Thr Ala Thr Phe Thr Asp Asn Ala Ser Val Thr
          145            150            155            160

Leu Gln Lys Asn Thr Ser Glu Lys Asp Gly Ala Ala Val Ser Ala Tyr
          165            170            175

Ser Ile Asp Leu Ala Lys Thr Thr Thr Ala Ala Leu Leu Asp Gln Asn
          180            185            190

Thr Ser Thr Lys Asn Gly Gly Ala Leu Cys Ser Thr Ala Asn Thr Thr
          195            200            205

Val Gln Gly Asn Ser Gly Thr Val Thr Phe Ser Ser Asn Thr Ala Thr
          210            215            220

Asp Lys Gly Gly Gly Ile Tyr Ser Lys Glu Lys Asp Ser Thr Leu Asp
          225            230            235            240

Ala Asn Thr Gly Val Val Thr Phe Lys Ser Asn Thr Ala Lys Thr Gly
          245            250            255

Gly Ala Trp Ser Ser Asp Asp Asn Leu Ala Leu Thr Gly Asn Thr Gln
          260            265            270

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46/55

Val Leu Phe Gln Glu Asn Lys Thr Thr Gly Ser Ala Ala Gln Ala Asn  
 275 280 285  
 Asn Pro Glu Gly Cys Gly Gly Ala Ile Cys Cys Tyr Leu Ala Thr Ala  
 290 295 300  
 Thr Asp Lys Thr Gly Leu Ala Ile Ser Gln Asn Gln Glu Met Ser Phe  
 305 310 315 320  
 Thr Ser Asn Thr Thr Thr Ala Asn Gly Gly Ala Ile Tyr Ala Thr Lys  
 325 330 335  
 Cys Thr Leu Asp Gly Asn Thr Thr Leu Thr Phe Asp Gln Asn Thr Ala  
 340 345 350  
 Thr Ala Gly Cys Gly Gly Ala Ile Tyr Thr Glu Thr Glu Asp Phe Ser  
 355 360 365  
 Leu Lys Gly Ser Thr Gly Thr Val Thr Phe Ser Thr Asn Thr Ala Lys  
 370 375 380  
 Thr Gly Gly Ala Leu Tyr Ser Lys Gly Asn Ser Ser Leu Thr Gly Asn  
 385 390 395 400  
 Thr Asn Leu Leu Phe Ser Gly Asn Lys Ala Thr Gly Pro Ser Asn Ser  
 405 410 415  
 Ser Ala Asn Gln Glu Gly Cys Gly Gly Ala Ile Leu Ala Phe Ile Asp  
 420 425 430  
 Ser Gly Ser Val Ser Asp Lys Thr Gly Leu Ser Ile Ala Asn Asn Gln  
 435 440 445  
 Glu Val Ser Leu Thr Ser Asn Ala Ala Thr Val Ser Gly Gly Ala Ile  
 450 455 460  
 Tyr Ala Thr Lys Cys Thr Leu Thr Gly Asn Gly Ser Leu Thr Phe Asp  
 465 470 475 480  
 Gly Asn Thr Ala Gly Thr Ser Gly Gly Ala Ile Tyr Thr Glu Thr Glu  
 485 490 495  
 Asp Phe Thr Leu Thr Gly Ser Thr Gly Thr Val Thr Phe Ser Thr Asn  
 500 505 510  
 Thr Ala Lys Thr Gly Gly Ala Leu Tyr Ser Lys Gly Asn Asn Ser Leu  
 515 520 525  
 Ser Gly Asn Thr Asn Leu Leu Phe Ser Gly Asn Lys Ala Thr Gly Pro  
 530 535 540  
 Ser Asn Ser Ser Ala Asn Gln Glu Gly Cys Gly Gly Ala Ile Leu Ser  
 545 550 555 560

47/55

Phe Leu Glu Ser Ala Ser Val Ser Thr Lys Lys Gly Leu Trp Ile Glu  
 565 570 575  
 Asp Asn Glu Asn Val Ser Leu Ser Gly Asn Thr Ala Thr Val Ser Gly  
 580 585 590  
 Gly Ala Ile Tyr Ala Thr Lys Cys Ala Leu His Gly Asn Thr Thr Leu  
 595 600 605  
 Thr Phe Asp Gly Asn Thr Ala Glu Thr Ala Gly Gly Ala Ile Tyr Thr  
 610 615 620  
 Glu Thr Glu Asp Phe Thr Leu Thr Gly Ser Thr Gly Thr Val Thr Phe  
 625 630 635 640  
 Ser Thr Asn Thr Ala Lys Thr Ala Gly Ala Leu His Thr Lys Gly Asn  
 645 650 655  
 Thr Ser Phe Thr Lys Asn Lys Ala Leu Val Phe Ser Gly Asn Ser Ala  
 660 665 670  
 Thr Ala Thr Ala Thr Thr Thr Thr Asp Gln Glu Gly Cys Gly Gly Ala  
 675 680 685  
 Ile Leu Cys Asn Ile Ser Glu Ser Asp Ile Ala Thr Lys Ser Leu Thr  
 690 695 700  
 Leu Thr Glu Asn Glu Ser Leu Ser Phe Ile Asn Asn Thr Ala Lys Arg  
 705 710 715 720  
 Ser Gly Gly Gly Ile Tyr Ala Pro Lys Cys Val Ile Ser Gly Ser Glu  
 725 730 735  
 Ser Ile Asn Phe Asp Gly Asn Thr Ala Glu Thr Ser Gly Gly Ala Ile  
 740 745 750  
 Tyr Ser Lys Asn Leu Ser Ile Thr Ala Asn Gly Pro Val Ser Phe Thr  
 755 760 765  
 Asn Asn Ser Gly Gly Lys Gly Gly Ala Ile Tyr Ile Ala Asp Ser Gly  
 770 775 780  
 Glu Leu Ser Leu Glu Ala Ile Asp Gly Asp Ile Thr Phe Ser Gly Asn  
 785 790 795 800  
 Arg Ala Thr Glu Gly Thr Ser Thr Pro Asn Ser Ile His Leu Gly Ala  
 805 810 815  
 Arg Gly Lys Ile Thr Lys Leu Ala Ala Ala Pro Gly His Thr Ile Tyr  
 820 825 830  
 Phe Tyr Asp Pro Ile Thr Met Glu Ala Pro Ala Ser Gly Gly Thr Ile  
 835 840 845  
 Glu Glu Leu Val Ile Asn Pro Val Val Lys Ala Ile Val Pro Pro Pro  
 850 855 860

48/55

Glu Asp Ser Ser Phe Gly Gly Gly Ile Phe Cys Arg Ala Val Asn Ile  
225 230 235 240



49/55

Glu Arg Asn Tyr Gln Asn Ile Gln Ile Asn Asp Asn Ala Ser Gly Gln  
 245 250 255  
 Gly Val Val Tyr Phe Leu Pro Leu Gly Val Ile Ile Ser Ser Asn Lys  
 260 265 270  
 Glu Ile Ile Glu Ile Ser Asn His Ser Ala Ser Ser Ile Asn Thr Ala  
 275 280 285  
 Ser Gly Lys Leu Tyr Pro Gly Gly Gly Gly Ile Met Cys Thr Ser Leu  
 290 295 300  
 Ser His Glu Asn Asn Pro Lys Gly Leu Ile Phe Asn Asn Lys Thr Ala  
 305 310 315 320  
 Ala Leu Ser Gly Gly Val Tyr Thr Arg Asp Leu Ser Ser Ser Lys Ile  
 325 330 335  
 Thr Val Arg Thr Ala Phe Ile Asn Asn Ser Ala Thr Ser Gly Gly Ala  
 340 345 350  
 Leu Ile Asn Leu Ser Gly Ile Gly Ser Thr Pro Gln Asn Phe Phe Leu  
 355 360 365  
 Ser Ala Asp Tyr Gly Asp Ile Leu Phe Asn Asn Asn Thr Ile Thr Ser  
 370 375 380  
 Ser Ser Pro Gln Pro Gly Tyr Arg Asn Ala Leu Tyr Ala Ala Pro Gly  
 385 390 395 400  
 Ile Asn Leu Lys Leu Gly Ala Arg Gln Gly Tyr Lys Ile Leu Phe Tyr  
 405 410 415  
 Asp Pro Ile Asp His Asp Gln Thr Thr Thr Asp Pro Ile Val Phe Asn  
 420 425 430  
 Tyr Glu Pro His His Leu Gly Thr Val Leu Phe Ser Gly Ile Asn Val  
 435 440 445  
 Asp Ser Asn Ala Thr Asn Pro Leu Asn Phe Leu Ser Lys Phe Ser Asn  
 450 455 460  
 Ser Ser Arg Leu Glu Arg Gly Val Leu Ala Ile Glu Asp Arg Ala Ala  
 465 470 475 480  
 Ile Ser Cys Lys Thr Leu Ser Gln Thr Gly Gly Ile Leu Arg Leu Gly  
 485 490 495  
 Asn Ala Ala Leu Ile Arg Thr Lys Gly Pro Gly Ser Ser Ile Asn Phe  
 500 505 510  
 Asn Ala Ile Ala Ile Asn Leu Pro Ser Ile Leu Gln Ser Glu Ala Ser  
 515 520 525

50/55

Ala Pro Lys Phe Trp Ile Tyr Pro Thr Leu Thr Gly Ser Thr Tyr Ser  
530 535 540

Glu Asp Thr Ser Ser Thr Ile Thr Leu Ser Gly Pro Leu Thr Phe Leu  
545 550 555 560

Asn Asp Glu Asn Glu Asn Pro Tyr Asp Ser Leu Asp Leu Ser Glu Pro  
565 570 575

Arg Lys Asp Ile Pro Pro Pro Leu Pro Pro Arg Cys Asp Cys Lys Lys  
580 585 590

Ile Asp Thr Ser Asn Leu Ile Val Glu Ala Met Asn Leu Asp Glu His  
595 600 605

Tyr Gly Tyr Gln Gly Ile Trp Ser Pro Tyr Trp Met Glu Thr Thr Thr  
610 615 620

Thr Thr Ser Ser Thr Val Pro Glu Gln Thr Asn Thr Asn His Arg Gln  
625 630 635 640

Leu Tyr Val Asp Trp Thr Pro Val Gly Tyr Arg Pro Asn Pro Glu Arg  
645 650 655

His Gly Glu Phe Ile Ala Asn Thr Leu Trp Gln Ser Ala Tyr Asn Ala  
660 665 670

Leu Leu Gly Ile Arg Ile Leu Pro Pro Gln Asn Leu Lys Glu His Asp  
675 680 685

Leu Glu Ala Ser Leu Gln Gly Leu Gly Leu Leu Ile Asn Gln His Asn  
690 695 700

Arg Glu Gly Arg Lys Gly Phe Arg Asn His Thr Thr Gly Tyr Ala Ala  
705 710 715 720

Thr Thr Ser Ala Lys Thr Ala Ala Arg His Ser Phe Ser Leu Gly Phe  
725 730 735

Ala Gln Met Phe Ser Lys Thr Arg Glu Arg Gln Ser Pro Ser Thr Thr  
740 745 750

Ser Ser His Asn Tyr Phe Ala Gly Leu Arg Phe Asp Ser Leu Leu Phe  
755 760 765

Arg Asp Phe Ile Ser Thr Gly Leu Ser Leu Gly Tyr Ser Tyr Gly Asp  
770 775 780

His His Met Leu Cys His Tyr Thr Glu Ile Leu Lys Gly Ser Ser Lys  
785 790 795 800

Ala Phe Phe Asn Asn His Thr Leu Val Ala Ser Leu Asp Cys Thr Phe  
805 810 815

Leu Pro Ala Arg Ile Thr Arg Thr Leu Glu Leu Gln Pro Phe Ile Ser  
820 825 830

51/55

Ala Ile Ala Leu Arg Cys Ser Gln Ala Ser Phe Gln Glu Thr Gly Asp  
 835 840 845

His Ile Arg Lys Phe His Pro Lys His Pro Leu Thr Asp Leu Ser Ser  
 850 855 860

Pro Ile Gly Phe Arg Ser Glu Trp Lys Thr Ser His His Ile Pro Met  
 865 870 875 880

Leu Trp Thr Thr Glu Ile Ser Tyr Val Pro Thr Leu Tyr Arg Lys Asn  
 885 890 895

Pro Glu Met Phe Thr Thr Leu Leu Ile Ser Asn Gly Thr Trp Thr Thr  
 900 905 910

Gln Ala Thr Pro Val Ser Tyr Asn Ser Val Ala Ala Lys Ile Lys Asn  
 915 920 925

Thr Ser Gln Leu Phe Ser Arg Val Thr Leu Ser Leu Asp Tyr Ser Ala  
 930 935 940

Gln Val Ser Ser Ser Thr Val Gly Gln Tyr Leu Lys Ala Glu Ser His  
 945 950 955 960

Cys Thr Phe

&lt;210&gt; 23

&lt;211&gt; 514

&lt;212&gt; PRT

&lt;213&gt; Chlamydia pneumoniae

&lt;400&gt; 23

Met Thr Ile Leu Arg Asn Phe Leu Thr Cys Ser Ala Leu Phe Leu Ala  
 1 5 10 15

Leu Pro Ala Ala Ala Gln Val Val Tyr Leu His Glu Ser Asp Gly Tyr  
 20 25 30

Asn Gly Ala Ile Asn Asn Lys Ser Leu Glu Pro Lys Ile Thr Cys Tyr  
 35 40 45

Pro Glu Gly Thr Ser Tyr Ile Phe Leu Asp Asp Val Arg Ile Ser Asn  
 50 55 60

Val Lys His Asp Gln Glu Asp Ala Gly Val Phe Ile Asn Arg Ser Gly  
 65 70 75 80

Asn Leu Phe Phe Met Gly Asn Arg Cys Asn Phe Thr Phe His Asn Leu  
 85 90 95

Met Thr Glu Gly Phe Gly Ala Ala Ile Ser Asn Arg Val Gly Asp Thr  
 100 105 110

52/55

Thr Leu Thr Leu Ser Asn Phe Ser Tyr Leu Ala Phe Thr Ser Ala Pro  
 115 120 125  
 Leu Leu Pro Gln Gly Gln Gly Ala Ile Tyr Ser Leu Gly Ser Val Met  
 130 135 140  
 Ile Glu Asn Ser Glu Glu Val Thr Phe Cys Gly Asn Tyr Ser Ser Trp  
 145 150 155 160  
 Ser Gly Ala Ala Ile Tyr Thr Pro Tyr Leu Leu Gly Ser Lys Ala Ser  
 165 170 175  
 Arg Pro Ser Val Asn Leu Ser Gly Asn Arg Tyr Leu Val Phe Arg Asp  
 180 185 190  
 Asn Val Ser Gln Val Tyr Gly Gly Ala Ile Ser Thr His Asn Leu Thr  
 195 200 205  
 Leu Thr Thr Arg Gly Pro Ser Cys Phe Glu Asn Asn His Ala Tyr His  
 210 215 220  
 Asp Val Asn Ser Asn Gly Gly Ala Ile Ala Ile Ala Pro Gly Gly Ser  
 225 230 235 240  
 Ile Ser Ile Ser Val Lys Ser Gly Asp Leu Ile Phe Lys Gly Asn Thr  
 245 250 255  
 Ala Ser Gln Asp Gly Asn Thr Ile His Asn Ser Ile His Leu Gln Ser  
 260 265 270  
 Gly Ala Gln Phe Lys Asn Leu Arg Ala Val Ser Glu Ser Gly Val Tyr  
 275 280 285  
 Phe Tyr Asp Pro Ile Ser His Ser Glu Ser His Lys Ile Thr Asp Leu  
 290 295 300  
 Val Ile Asn Ala Pro Glu Gly Lys Glu Thr Tyr Glu Gly Thr Ile Ser  
 305 310 315 320  
 Phe Ser Gly Leu Cys Leu Asp Asp His Glu Val Cys Ala Glu Asn Leu  
 325 330 335  
 Thr Ser Thr Ile Leu Gln Asp Val Thr Leu Ala Gly Gly Thr Leu Ser  
 340 345 350  
 Leu Ser Asp Gly Val Thr Leu Gln Leu His Ser Phe Lys Gln Glu Ala  
 355 360 365  
 Ser Ser Thr Leu Thr Met Ser Pro Gly Thr Thr Leu Leu Cys Ser Gly  
 370 375 380  
 Asp Ala Arg Val Gln Asn Leu His Ile Leu Ile Glu Asp Thr Asp Asn  
 385 390 395 400  
 Phe Val Pro Val Arg Ile Arg Ala Glu Asp Lys Asp Ala Leu Val Ser  
 405 410 415

53/55

Leu Glu Lys Leu Lys Val Ala Phe Glu Ala Tyr Trp Ser Val Tyr Asp  
 420 425 430

Phe Pro Gln Phe Lys Glu Ala Phe Thr Ile Pro Leu Leu Glu Leu Leu  
 435 440 445

Gly Pro Ser Phe Asp Ser Leu Leu Leu Gly Glu Thr Thr Leu Glu Arg  
 450 455 460

Thr Gln Val Thr Thr Glu Asn Asp Ala Val Arg Gly Phe Trp Ser Leu  
 465 470 475 480

Ser Trp Glu Glu Tyr Pro Pro Ser Leu Asp Lys Asp Arg Arg Ile Thr  
 485 490 495

Pro Thr Lys Lys Thr Val Phe Leu Thr Trp Asn Pro Glu Ile Thr Ser  
 500 505 510

Thr Pro

<210> 24  
 <211> 289  
 <212> PRT  
 <213> Chlamydia pneumoniae

&lt;400&gt; 24

Met Gly Ile Ser Leu Pro Glu Leu Phe Ser Asn Leu Gly Ser Ala Tyr  
 1 5 10 15

Leu Asp Tyr Ile Phe Gln His Pro Pro Ala Tyr Val Trp Ser Val Phe  
 20 25 30

Leu Leu Leu Leu Ala Arg Leu Leu Pro Ile Phe Ala Val Ala Pro Phe  
 35 40 45

Leu Gly Ala Lys Leu Phe Pro Ser Pro Ile Lys Ile Gly Ile Ser Leu  
 50 55 60

Ser Trp Leu Ala Ile Ile Phe Pro Lys Val Leu Ala Asp Thr Gln Ile  
 65 70 75 80

Thr Asn Tyr Met Asp Asn Asn Leu Phe Tyr Val Leu Leu Val Lys Glu  
 85 90 95

Met Ile Ile Gly Ile Val Ile Gly Phe Val Leu Ala Phe Pro Phe Tyr  
 100 105 110

Ala Ala Gln Ser Ala Gly Ser Phe Ile Thr Asn Gln Gln Gly Ile Gln  
 115 120 125

Gly Leu Glu Gly Ala Thr Ser Leu Ile Ser Ile Glu Gln Thr Ser Pro  
 130 135 140

54/55

His Gly Ile Leu Tyr His Tyr Phe Val Thr Ile Ile Phe Trp Leu Val  
145 150 155 160

Gly Gly His Arg Ile Val Ile Ser Leu Leu Leu Gln Thr Leu Glu Val  
165 170 175

Ile Pro Ile His Ser Phe Phe Pro Ala Glu Met Met Ser Leu Ser Ala  
180 185 190

Pro Ile Trp Ile Thr Met Ile Lys Met Cys Gln Leu Cys Leu Val Met  
195 200 205

Thr Ile Gln Leu Ser Ala Pro Ala Ala Leu Ala Met Leu Met Ser Asp  
210 215 220

Leu Phe Leu Gly Ile Ile Asn Arg Met Ala Pro Gln Val Gln Val Ile  
225 230 235 240

Tyr Leu Leu Ser Ala Leu Lys Ala Phe Met Gly Leu Leu Phe Leu Thr  
245 250 255

Leu Ala Trp Trp Phe Ile Ile Lys Gln Ile Asp Tyr Phe Thr Leu Ala  
260 265 270

Trp Phe Lys Glu Val Pro Ile Met Leu Leu Gly Ser Asn Pro Gln Val  
275 280 285

Leu

<210> 25

<211> 265

<212> PRT

<213> Chlamydia pneumoniae

<400> 25

Met Lys His Ser Lys Glu Asp Asp Leu Ser Arg Phe Leu Pro Lys Asn  
1 5 10 15

Leu Leu Val Glu Ser Pro His Pro Glu Glu Ile Pro Leu Lys Ser Leu  
20 25 30

Ser Phe Thr Met Ser Trp Leu Pro Thr Ile His Pro Ser Trp Ile Thr  
35 40 45

Ile Ala Met Lys Glu Phe Pro Pro Glu Ile Gln Gly Gln Leu Leu Ala  
50 55 60

Trp Leu Pro Glu Pro Leu Val Gln Glu Ile Leu Pro Leu Leu Pro Gly  
65 70 75 80

Ile Ser Ile Ala Pro His Arg Cys Ala Pro Phe Gly Ala Phe Tyr Leu  
85 90 95

Leu Asp Met Leu Ser Lys Lys Ile Arg Pro Cys Gly Ile Thr Glu Glu  
100 105 110

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55/55

Ile Phe Leu Pro Ala Ser Ser Ala Asn Ala Ile Leu Tyr Tyr Thr Gly  
 115 120 125  
 Pro Val Lys Ile Ala Leu Ile Asn Cys Leu Gly Leu Tyr Ser Ile Ala  
 130 135 140  
 Lys Glu Leu Lys His Ile Leu Asp Lys Val Val Ile Glu Arg Val Lys  
 145 150 155 160  
 Asn Ala Leu Ser Pro Thr Glu Lys Leu Phe Leu Thr Tyr Cys Gln Ser  
 165 170 175  
 His Pro Met Lys His Leu Glu Thr Thr Asn Phe Leu Ser Ser Trp Thr  
 180 185 190  
 Thr Asp Ala Glu Leu Arg Gln Phe Val His Lys Gln Gly Leu Glu Phe  
 195 200 205  
 Leu Gly Lys Ala Leu Thr Lys Glu Asn Ala Ser Phe Leu Trp Tyr Phe  
 210 215 220  
 Leu Arg Arg Leu Asp Val Gly Arg Ala Tyr Ile Val Glu Gln Thr Leu  
 225 230 235 240  
 Lys Thr Trp Tyr Asp His Pro Tyr Val Asp Tyr Phe Lys Ser Arg Leu  
 245 250 255  
 Glu Gln Cys Met Lys Val Leu Val Lys  
 260 265  
 <210> 26  
 <211> 95  
 <212> PRT  
 <213> Chlamydia pneumoniae  
 <400> 26  
 Met Leu Ala Phe Phe Ala Thr Ser Phe Lys Ser Val Leu Phe Glu Tyr  
 1 5 10 15  
 Ser Tyr Gln Ser Leu Leu Leu Ile Leu Ile Val Ser Ala Pro Pro Ile  
 20 25 30  
 Ile Leu Ala Ser Ile Val Gly Ile Met Val Ala Ile Phe Gln Ala Ala  
 35 40 45  
 Thr Gln Ile Gln Glu Gln Thr Phe Ala Phe Ala Val Lys Leu Val Val  
 50 55 60  
 Ile Phe Gly Thr Leu Met Ile Ser Gly Gly Trp Leu Ser Asn Met Ile  
 65 70 75 80  
 Leu Arg Phe Ala Gly Gln Ile Phe Gln Asn Phe Tyr Lys Trp Lys  
 85 90 95